



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 105234

TO: Phillip Gambel
Location: CM1/8B03&9E12
Art Unit: 1644
Wednesday, October 08, 2003

Case Serial Number: 09/730466

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Gambel,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6
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M protein - protein search, using sw model

un on: October 7, 2003, 11:09:47 ; Search time 83 Seconds
(without alignments)
175.938 Million cell updates/sec

Title: US-09-730-465-2_COPY_1_92

Perfect score: 475

Sequence: 1 MWAGSDAGRALGVLSVVCLL.....AFSSFKRVYLDVTYSGSLTI 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

- 1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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- 10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475	100.0	112	ABB81992	Human transmembran
2	475	100.0	120	AA027157	LFA-3 CD2 binding
3	475	100.0	128	AA04361	Human cell adhesio
4	475	100.0	133	AA04362	Human cell adhesio
5	475	100.0	133	AA04363	Human cell adhesio
6	475	100.0	237	AA020804	Human LFA-3 antige
7	475	100.0	237	AA091432	Human LFA-3 antige
8	475	100.0	237	AA080441	Human LFA-3 antige
9	475	100.0	237	AA086189	Human LFA-3 antige

10	475	100.0	237	AA096127	Human cell surface
11	475	100.0	237	AA02436	Human lymphocyte f
12	475	100.0	240	AA05572	PI-linked LFA-3 em
13	475	100.0	240	AA07604	Lymphocyte functio
14	475	100.0	240	AA07162	PI-linked LFA-3 us
15	475	100.0	240	AA083134	PI-linked human tr
16	475	100.0	240	AA061158	Human PI-linked tr
17	475	100.0	240	AA076226	PI-linked lymphocy
18	475	100.0	250	AA081507	Human LFA-3 expres
19	475	100.0	250	AA07161	Transmembrane LFA-
20	475	100.0	250	AA04371	Sequence encoded b
21	475	100.0	250	AA064271	Human LFA-3. Homo
22	475	100.0	250	AA04370	Human cell adhesio
23	475	100.0	250	AA083133	Human transmembran
24	475	100.0	250	AA061157	Human transmembran
25	475	100.0	250	AA076225	Lymphocyte functio
26	475	100.0	256	AA016017	Murine CD2-binding
27	475	100.0	347	AA027163	CD2 binding LFA-3-
28	475	100.0	347	AA083136	Human transmembran
29	475	100.0	347	AA061160	Human LFA3TIP fusi
30	475	100.0	347	AB070766	Human lymphocyte f
31	475	100.0	347	AB081994	Human LFA3TIP poly
32	475	100.0	347	AA076228	LFA3/IgG fusion pr
33	475	100.0	347	AB058178	Murine LFA-3. Mus
34	475	100.0	351	AB081995	Human LFA-3/IgG fu
35	472	99.4	240	AA034222	Amino acid sequenc
36	472	99.4	240	AA034372	Sequence encoded b
37	472	99.4	250	AA034221	Amino acid sequenc
38	469	98.7	237	AA016687	Human CD58 GPI. H
39	464	97.7	237	AA014182	Human LFA-3(CD58)
40	463	97.5	347	AA034224	Amino acid sequenc
41	459	96.6	250	AA028365	Human LFA-3 protei
42	443	93.3	280	AB018595	Novel human diagno
43	328	69.1	71	AA037158	LFA-3 CD2 binding
44	328	69.1	134	AA028364	Human LFA-3 D2 reg
45	328	69.1	135	AA028369	Human LFA-3-delta-

ALIGNMENTS

RESULT 1
ABB81992 standard; Protein; 112 AA.
XX ABB81992;
XX
XX 25-NOV-2002 (first entry)
XX Human transmembrane LFA-3 partial polypeptide.

Human; immunosuppressive; antitumor; dermatological; antineoplastic; antiproliferative; antipneumatic; antirheumatic; antidiabetic; gene therapy; CD2; LFA-3; interferon; IFN; osteopontin; CD8; CD45.

Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..28 /note= "signal peptide"
XX Protein 29..84 /note= "partial mature protein fragment; the sequence after position 84 is not indicated in the specification; the pages containing the complete sequence are not provided"

WO200260480-A1.

08-AUG-2002.

25-JAN-2002; 2002WO-US02314.

R 01-FEB-2001; 2001US-265964P.

X (BIOJ) BIOGEN INC.

X Vaishnav AK, Cooper KD, Shrager D, McCormick TS;

X WPI; 2002-657488/70.

R N-PSDB; ABQ79655.

X Treating or preventing, by inhibiting CD2/LFA-3 interaction, an
T epidermal or dermal disorder, inflammatory and/or autoimmune disorder
T with aberrant T cell activity or proliferation -

X Disclosure; Page 58; 68pp; English.

X The invention relates to treating or preventing an epidermal or dermal
C disorder, an inflammatory disorder and/or an autoimmune disorder in a
C subject with aberrant T cell activity or proliferation. The method
C involves administering an inhibitor of the CD2/LFA-3 interaction, in
C combination with an auxiliary agent, thereby treating or preventing the
C epidermal or dermal disorder, the inflammatory disorder or the autoimmune
C disorder. The methods and compositions of the invention are useful for
C preventing or treating skin disorders characterized by increased T cell
C activation and abnormal antigen presentation in the dermis and epidermis,
C such as psoriasis, UV damage, atopic dermatitis, cutaneous T cell
C lymphoma, contact and atopic dermatitis, lichen planus, alopecia,
C vitiligo, urticaria. They may also be used in chronic inflammatory and
C autoimmune disorders such as diabetes mellitus, arthritis, rheumatoid
C arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
C arthritis, multiple sclerosis, encephalomyelitis, myasthenia gravis,
C systemic lupus erythematosus, autoimmune thyroiditis. The present
C sequence represents the human transmembrane LFA-3 partial amino acid
C sequence.

SQ Sequence 112 AA;

Query Match 100.0%; Score 475; DB 23; Length 112;

Best Local Similarity 100.0%; Pred. No. 4.5e-51;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWAGDAGRALGVLSVCLLHCFGFCISFCSQIYGVVGNVTHVPSNVLKVLKKQK 60

DB 1 MWAGDAGRALGVLSVCLLHCFGFCISFCSQIYGVVGNVTHVPSNVLKVLKKQK 60

QY 61 DKVAELENSEFRASFKNRYLDVTSGSLTI 92

DB 61 DKVAELENSEFRASFKNRYLDVTSGSLTI 92

RESULT 2

AAAR27157

ID AAR27157 standard; protein; 120 AA.

XX AAR27157;

AC AAR27157;

XX 25-MAR-2003 (updated)

DT 20-MAY-1998 (first entry)

XX LFA-3 CD2 binding domain polypeptide #2.

DE Lymphocyte associated antigen-3; T-lymphocyte accessory molecule.

XX Synthetic.

OS Key

XX Location/Qualifiers

FT 2..78

FT /note= "1-77 of these residues may be deleted"

FT 89..120

FT /note= "1-32 of these residues may be deleted"

FT

XX EF503648-A1.

PN 16-SEP-1992.

XX

PD

XX 12-MAR-1992; 92EP-0104320.

XX 12-MAR-1991; 91US-0667971.

PR 07-OCT-1991; 91US-0770967.

XX (BIOJ) BIOGEN INC.

PA Miller GT, Rosa MD, Wallner BP;

PI WPI; 1992-309760/38.

XX CD2-binding domain of lymphocyte function associated antigen-3

XX and DNA - for diagnosing and treating inflammation and

XX auto-immune diseases, e.g. systemic lupus erythematosus and

XX rheumatoid arthritis

XX Claim 1; Page 52-53; 85pp; English.

XX This polypeptide can bind to CD2. The N-terminal Met is opt.

XX absent. The N-terminal and C-terminal portions can be deleted.

XX The polypeptide and its functional deletion mutants may be used to

XX treat acute and chronic inflammation, autoimmune disease and for

XX immunomodulation. The polypeptides can also form the N-terminal

XX part of a fusion protein. The polypeptides and fusion proteins may

XX also be used to inhibit T-cell activation and the proliferation of

XX peripheral blood lymphocytes. Multimeric proteins can be formed from

XX the polypeptides and/or fusion proteins. The multimers have enhanced

XX affinity for CD2. See also AAR27157-9.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 120 AA;

Query Match 100.0%; Score 475; DB 13; Length 120;

Best Local Similarity 100.0%; Pred. No. 4.9e-51;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWAGDAGRALGVLSVCLLHCFGFCISFCSQIYGVVGNVTHVPSNVLKVLKKQK 60

DB 1 MWAGDAGRALGVLSVCLLHCFGFCISFCSQIYGVVGNVTHVPSNVLKVLKKQK 60

QY 61 DKVAELENSEFRASFKNRYLDVTSGSLTI 92

DB 61 DKVAELENSEFRASFKNRYLDVTSGSLTI 92

RESULT 3

AAAW04361

ID AAW04361 standard; protein; 128 AA.

XX AAW04361;

XX 27-JUN-1997 (first entry)

XX Human cell adhesion protein LFA-3.

DE Human; T cell; MOLT-4; cell adhesion; LFA-3; immunosuppression;

XX cell line; immunosuppressant cell.

XX Homo sapiens.

OS WO9633217-A1.

XX 24-OCT-1996.

XX 15-APR-1996; 96WO-JP01039.

XX 27-DEC-1995; 95JP-0341959.

XX 19-APR-1995; 95JP-0094060.

XX 04-JUL-1995; 95JP-0169110.

XX (KANF) KANEGAFUCHI KAGAKU KOGYO KK.

XX

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M protein - protein search, using sw model

un on: October 7, 2003, 11:13:47 ; Search time 40 Seconds
(without alignments)
221.188 Million cell updates/sec

title: us-09-730-465-2_copy_1_92

perfect score: 475
sequence: 1 MVAGSDAGRALGVLSVCL.....AFSSFKNRVLDTVSGSLTI 92

scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	475	100.0	250	2 A28564	lymphocyte functio
2	74.5	15.7	243	2 A53244	leukocyte antigen
3	70	14.7	546	2 T25568	hypothetical prote
4	69.5	14.6	389	2 T16326	hypothetical prote
5	67.5	14.2	240	2 JL0143	antigen BCM1 precu
6	66	13.9	661	2 S49901	coat protein gpl -
7	66	13.9	707	2 JC7763	neuronal leucine-r
8	65	13.7	416	2 T25036	hypothetical prote
9	65	13.7	1822	2 S44849	K12H4.8 protein -
10	64	13.5	737	2 T13504	NADH2 dehydrogenas
11	63.5	13.4	562	2 C82355	hypothetical prote
12	63	13.3	234	2 AD1649	weakly phage relat
13	63	13.3	299	2 E90162	conserved hypothet
14	63	13.3	608	2 S58091	probable membrane
15	62.5	13.2	274	2 S76154	hypothetical prote
16	62.5	13.2	655	2 T23874	hypothetical prote
17	62.5	13.2	734	2 T13685	NADH2 dehydrogenas
18	62	13.1	237	2 C70157	hypothetical prote
19	62	13.1	403	2 C33958	hypothetical prote
20	62	13.1	414	2 H84936	tRNA adenylyltrans
21	62	13.1	426	2 A81933	probable malate de
22	62	13.1	426	2 C81173	malate oxidoreduct
23	62	13.1	510	2 E70321	GMP synthase (glut
24	61.5	12.9	522	2 E82024	peptide methionine
25	61.5	12.9	522	2 G81243	peptide methionine
26	61.5	12.9	741	2 T12711	NADH2 dehydrogenas
27	61.5	12.9	752	2 H71911	uncharacterized pr
28	61.5	12.9	836	2 E97851	hypothetical prote
29	61	12.8	344	2 T00993	probable beta-1,3-

T-cell surface gly
methionine adenosy
ornithine-oxo-acid.
dolichyl-diphospho
hypothetical prote
myosin I heavy cha
signal peptidase-1
alpha-1,2-galactos
probable acyl-CoA
hypothetical prote
protoporphyrinogen
centaurin, delta 2
variant-specific s
glycine receptor b
glycine receptor b
alpha-N-acetylglala

ALIGNMENTS

RESULT 1

A28564
lymphocyte function-associated antigen 3, transmembrane splice form precursor - huma
N:Alternate names: CD58 antigen; surface glycoprotein LFA-3
C:Species: Homo sapiens (man)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 02-Aug-2002
C:Accession: A28564; S01269
R:Wallner, B.P.; Frey, A.Z.; Tizard, R.; Mattaliano, R.J.; Hession, C.; Sanders, M.F
J. Exp. Med. 166, 923-932, 1987
A:Title: Primary structure of lymphocyte function-associated antigen 3 (LFA-3). The
A:Reference number: A28564; MUID:88009714; PMD:3309127
A:Accession: A28564
A:Molecule type: mRNA
A:Residues: 1-250 <WAL>
A:Cross-references: GB:X00636; NID:g34346; PIDN:CAA68668.1; PID:g34347
A:Experimental source: erythrocytes
A:Note: the authors translated the codon TAT for residue 34 as Val
R:Seed, B.
Nature 329, 840-842, 1987
A:Title: An LFA-3 CDNA encodes a phospholipid-linked membrane protein homologous to
A:Reference number: S01269; MUID:88039074; PMD:3313052
A:Accession: S01269
A:Molecule type: mRNA
A:Residues: 1-235, 'VL' <SEE>
A:Cross-references: EMBL:X06296; NID:g34349; PIDN:CAA29622.1; PID:g34350
C:Comment: For an alternative splice form, see PIR:S01269.
C:Comment: For an alternative splice form, see PIR:A28564.
C:Genetics:
A:Gene: GDB:CD58; LFA3
A:Cross-references: GDB:120580; OMIM:153420
A:Map position: lpi3-lpi3
C:Superfamily: human B-cell antigen CD19; immunoglobulin homology
C:Keywords: alternative splicing; glycoprotein; phosphatidylinositol linkage; surfac
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-250/Product: lymphocyte function-associated antigen 3 transmembrane splice form
F:135-189/Domain: immunoglobulin homology <IM>
F:40,94,109,135,169,195/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 100.0%; Score 475; DB 2; Length 250;

Best Local Similarity 100.0%; Pred. No. 2.3e-45;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAGSDAGRALGVLSVCLLCFCGFI SCFSQQIYGVYGVNVTFFHVP SNVPLKEV LKKOK 60
|||||
Db 1 MVAGSDAGRALGVLSVCLLCFCGFI SCFSQQIYGVYGVNVTFFHVP SNVPLKEV LKKOK 60
|||||

QY 61 DKVAELENSEFPASFSEKRNRYLDTVSGSLTI 92
|||||

Db 61 DKVAELENSEFPASFSEKRNRYLDTVSGSLTI 92
|||||

RESULT 2

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

R;White, S.

C;Accession: T26568

submitted to the EMBL Data Library, September 1999

A;Reference number: Z20234

A;Accession: T26568

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-546 <WIL>

A;Cross-references: EMBL:AL110478; NID:e1542139; PIDN:CAB54346.1; CESP:Y26D4A.10

A;Experimental source: clone Y26D4A

C;Genetics:

A;Gene: CESP:Y26D4A.10

A;Introns: 415/3; 506/3

Query Match 14.7%; Score 70; DB 2; Length 546;

Best Local Similarity 28.9%; Pred. No. 8.2; Mismatches 11; Indels 16; Gaps 3;

Matches 22; Conservative 11

QY 19 LLHCGFGTSCFOQIYGVY-----GNVTHVPSNPVLKEVLWKQ--KDKV-- 63

Db 163 LTHIFGFCVCKIYGRKKMLSLYSPENKNSITSSNPQNTAKWINKLQWIIPKIIP 222

QY 64 -AELENSEFEASF 78

Db 223 CLEMQKLLNIFESNK 238

RESULT 4

TI6326

hypothetical protein F41C6.7 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C;Accession: TI6326

R;Geisels, C.

submitted to the EMBL Data Library, October 1995

A;Description: The sequence of *C. elegans* cosmid F41C6.

A;Reference number: Z18495

A;Accession: TI6326

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-389 <GEI>

A;Cross-references: EMBL:U39745; NID:gl049470; PID:gl049476; PIDN:AAA80448.1; CESP:E4

C;Genetics:

A;Gene: CESP:F41C6.7

A;Introns: 50/3; 118/3; 136/3; 154/3; 189/3; 209/3; 235/2; 264/2; 300/3; 327/3; 362/3

Query Match 14.6%; Score 69.5; DB 2; Length 389;

Best Local Similarity 28.3%; Pred. No. 6.4; Mismatches 14; Indels 1; Gaps 1;

Matches 17; Conservative 14

QY 14 LSVGCLLHCFGFI SCFOQIYGVYGNVTHVPSNPVLKEVLWKQKQKVALENSFEPA 73

Db 289 LVAVCAIHSYWKLISSNMQSFIVIGYITHV-GNKAIVETICEVENQONRETIQSFSA 347

RESULT 5

JL0143

antigen BCM1 precursor - mouse

N;Alternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen

C;Species: *Mus musculus* (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Jan-2000

C;Accession: JL0143; S21319; A47469; B47469

R;Wong, Y.W.; Williams, A.F.; Kingmsmore, S.F.; Seidin, M.F.

J. Exp. Med. 171, 2115-2130, 1990

A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1) region on mouse chromosome 3.

A;Reference number: JL0143; MUID:90278362; PMID:1593656

A;Accession: JL0143

A;Molecule type: mRNA

A;Residues: 1-240 <WON>

A;Cross-references: EMBL:X17501; NID:g50134; PIDN:CAA35542.1; PID:g50135

R;Wong, Y.W.; Williams, A.F.; Kingmsmore, S.F.; Seidin, M.F.

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OM protein - protein search, using sw model

Run on: October 7, 2003, 11:12:57 ; Search time 22 Seconds
(without alignments)
196.657 Million cell updates/sec

Title: US-09-730-465-2_COPY_1_92
Perfect score: 475
Sequence: 1 MVAGSDAGRALGVLSVCLL.....AFSPKRNVLDTVSGSLTI 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475	100.0	250	1 LFA3_HUMAN	P19256 homo sapien
2	74.5	15.7	243	1 CD48_HUMAN	P09326 homo sapien
3	67.5	14.2	240	1 CD48_MOUSE	P18181 mus musculus
4	63.5	13.4	611	1 GLMS_WIGER	Q8d3j0 w mus musculus
5	63	13.3	379	1 ASPN_HUMAN	Q9bxx1 homo sapien
6	62	13.1	414	1 CCA_BUCAL	P57169 buchnera ap
7	62	13.1	461	1 PUCQ_RHOCA	P23462 rhodobacter
8	62	13.1	552	1 GUAA_AQAE	O66601 aquifex aeo
9	62	13.1	552	1 YHJL_SCHPO	Q9c0v8 schizosacch
10	61.5	12.9	522	1 MSAB_NEZGO	P14930 n peptide m
11	61.5	12.9	522	1 MSAB_NEIMA	Q9jwm8 n peptide m
12	61.5	12.9	522	1 MSAB_NEIMB	Q9kin8 n peptide m
13	61.5	12.9	741	1 NF5C_CICIN	Q32007 cichorium i
14	61	12.8	347	1 CD2_HORSE	P37998 equus cabal
15	61	12.8	373	1 ASPN_MOUSE	Q9nmg4 mus musculus
16	61	12.8	408	1 METK_DRONE	P40320 drosophila
17	61	12.8	424	1 ONT_FEAST	P07991 saccharomyc
18	61	12.8	508	1 GSPB_CHICK	P12244 gallus gall
19	61	12.8	1107	1 MYLE_RAT	O63356 rattus norv
20	60.5	12.7	193	1 Y304_SUITO	Q975x4 sulfobolus
21	60.5	12.7	262	1 Y931_STRPY	Q9a049 streptococ
22	60.5	12.7	490	1 YAM7_SCHPO	O10062 schizosacch
23	60.5	12.7	1136	1 CRD2_HUMAN	Q96948 homo sapien
24	60	12.6	496	1 GRB_MOUSE	P48168 mus musculus
25	60	12.6	496	1 GRB_RAT	P20781 rattus norv
26	60	12.6	526	1 S7A_MOUSE	Q9qz39 mus musculus
27	59.5	12.5	609	1 RFAL_XENLA	Q01388 xenopus lae
28	59.5	12.5	741	1 NF5C_ASTCO	P51097 aster cordi
29	59.5	12.5	974	1 ATXB_LEIDO	P12522 leishmania
30	59.5	12.5	1656	1 ATC8_YEAST	Q12674 saccharomyc
31	59	12.4	268	1 ILLA_BOVIN	P08381 bos taurus
32	59	12.4	288	1 CD80_HUMAN	P33681 homo sapien
33	59	12.4	314	1 TSPH_HABIN	P44976 haemophilus

34	59	12.4	438	1 ARLY_CLOTE	P59616 clostridium
35	59	12.4	511	1 GUAA_CAMJE	Q9pn49 campylobact
36	59	12.4	741	1 NUSC_FLARA	Q32238 flavaria ra
37	59	12.4	1109	1 MYLE_HUMAN	Q12965 homo sapien
38	58.5	12.3	165	1 GCSH_ARATH	P25855 arabidopsis
39	58.5	12.3	210	1 SODF_SULSO	P80857 sulfolobus
40	58.5	12.3	348	1 Y258_HELPV	P56136 helicobacte
41	58.5	12.3	351	1 MURG_HABIN	P45065 haemophilus
42	58.5	12.3	447	1 ANCA_CLOTH	Q66848 clostridium
43	58.5	12.3	508	1 GUAA_HELPV	Q92kg4 helicobacte
44	58.5	12.3	1069	1 ENTK_MOUSE	P97435 mus musculu
45	58	12.2	631	1 EMF2_ARATH	Q81674 arabidopsis

ALIGNMENTS

RESULT 1
LFA3_HUMAN
ID LFA3_HUMAN STANDARD; PRT; 250 AA.
AC P19256; Q96KI9;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lymphocyte function-associated antigen 3 precursor (Ag3) (Antigen
CD58) (Surface glycoprotein LFA-3).
GN CD58 OR LFA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RC TISSUE=Erythrocyte;
RX MEDLINE=88009714; PubMed=3309127;
RA Wallner B.P., Frey A.Z., Tizard R., Mattaliano R.J., Hession C.,
Sanders M.E., Dustin M.L., Springer T.A.;
RT "Primary structure of lymphocyte function-associated antigen 3 (LFA-
3). The ligand of the T lymphocyte CD2 glycoprotein.";
RL J. Exp. Med. 166:923-932(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=88039074; PubMed=3313052;
RA Seed B.;
RT "An LFA-3 cDNA encodes a phospholipid-linked membrane protein
homologous to its receptor CD2.";
RL Nature 329:840-842(1987).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=98169008; PubMed=9510189;
RA Wallich R., Brenner C., Brand Y., Roux M., Reister M., Meuer S.;
RT "Gene structure, promoter characterization, and basis for alternative
mRNA splicing of the human CD58 gene.";
RL J. Immunol. 160:2862-2871(1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 29-122.
RX MEDLINE=99218273; PubMed=10200255;
RA Ikemizu S., Sparks L.M., van der Merwe P.A., Harlos K., Stuart D.I.,
Jones E.Y., Davis S.J.;
RT "Crystal structure of the CD2-binding domain of CD58 (lymphocyte
function-associated antigen 3) at 1.8-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:4289-4294(1999).
CC -!- FUNCTION: LIGAND OF THE T LYMPHOCYTE CD2 GLYCOPROTEIN. THIS
INTERACTION IS IMPORTANT IN MEDIATING THYMOCYTE INTERACTIONS WITH
THYMIC EPITHELIAL CELLS, ANTIGEN-INDEPENDENT AND -DEPENDENT
INTERACTIONS OF T LYMPHOCYTES WITH TARGET CELLS AND ANTIGEN-
PRESENTING CELLS AND THE T LYMPHOCYTE ROSETTING WITH ERYTHROCYTES.
IN ADDITION, THE LFA-3/CD2 INTERACTION MAY PRIME RESPONSE BY BOTH
THE CD2+ AND LFA-3+ CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and
attached to the membrane by a GPI-anchor (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;

C Name=Long;
C IsoId=PI9256-1; Sequence=Displayed;
C Name=Short;
C IsoId=PI9256-2; Sequence=VSP_002522, VSP_002523;
C -I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
C -I- DATABASE: NAME=PROW; NOTE=CD guide CD58 entry;
C WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd58.htm".
C -----
C This SWISS-PROT entry is copyright. It is produced through a collaboration
C between the Swiss Institute of Bioinformatics and the EMBL outstation
C the European Bioinformatics Institute. There are no restrictions on its
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C entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
C or send an email to license@isb-sib.ch).
C -----
C
C EMBL: Y00636; CAA68668.1; -
C EMBL: X06296; CAA29622.1; -
C EMBL: Y14780; CAA75083.1; -
C EMBL: Y14781; CAA75083.1; JOINED.
C EMBL: Y14782; CAA75083.1; JOINED.
C EMBL: Y14783; CAA75083.1; JOINED.
C EMBL: Y14784; CAA75083.1; JOINED.
C EMBL: Y14780; CAA75084.1; -
C EMBL: Y14781; CAA75084.1; JOINED.
C EMBL: Y14782; CAA75084.1; JOINED.
C EMBL: Y14783; CAA75084.1; JOINED.
C EMBL: Y14784; CAA75084.1; JOINED.
C EMBL: Y14785; CAA75084.1; JOINED.
C PIR: A28564; A28564.
C PDB: 1CCZ; 05-APR-99.
C PDB: 1CI5; 22-JUN-99.
C Genew: HGNC:1688; CD58.
C MTM: 153420; -
C GO: GO:0005887; C-integral to plasma membrane; NAS.
C GO: GO:0005515; P:protein binding activity; IPI.
C GO: GO:0016337; P:cell-cell adhesion; NAS.
C InterPro: IPR003599; IG.
C SMART: SM00409; IG; 1.
C Alternative splicing: 3D-structure.
C
C IMMUNOGLOBULIN domain; Glycoprotein; Transmembrane; Signal; GPI-anchor;
C
C SIGNAL 1 28
C CHAIN 29 250
C DOMAIN 29 238
C TRANSMEM 216 238
C DOMAIN 239 250
C DOMAIN 135 194
C DISULFID 142 187
C CARBOHYD 40 40
C CARBOHYD 94 94
C CARBOHYD 109 109
C CARBOHYD 135 135
C CARBOHYD 169 169
C CARBOHYD 195 195
C VARSPLIC 236 237
C
C VARSPLIC 238 250
C
C SEQUENCE 250 AA; 28147 MW; 34D635DFD14FE2E CRC64;
C
C Query Match 100.0%; Score 475; DB 1; Length 250;
C Best Local Similarity 100.0%; Pred. No. 1.7e-45;
C Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
C
C 1 MVAGSAGALGVLSVCLLCFGISFCISQITGVYGNVTFHVPNSVPLKEVLKKQK 60
C |||||
C 1 MVAGSAGALGVLSVCLLCFGISFCISQITGVYGNVTFHVPNSVPLKEVLKKQK 60
C |||||
C 61 DKVAELNESEFRASFKNRVYLDVPSGLTI 92
C |||||
C 61 DKVAELNESEFRASFKNRVYLDVPSGLTI 92

RESULT 2
CD48_HUMAN
ID CD48_HUMAN STANDARD; PRT; 243 AA.
AC P09326;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE B-lymphocyte activation marker BLAST-1 precursor (BCM1 surface
DE antigen) (Leucocyte antigen MEM-102) (TCT.1) (Antigen CD48).
GN CD48 OR BCM1 OR BLAST1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91153858; PubMed-1999351;
RA Vaughan H.A., Henning M.M., Furcell D.F.J., McKenzie I.F.C.,
RA Sandrin M.S.;
RT "The isolation of cDNA clones for CD48";
RL Immunogenetics 33:113-117(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91153857; PubMed-1999350;
RA Korinek V., Stefanova I., Angelisova P., Hilbert I., Horejsi V.;
RA "The human leucocyte antigen CD48 (MEM-102) is closely related to the
RA activation marker Blast-1";
RT Immunogenetics 33:108-112(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-88111558; PubMed-2828034;
RA Staunton D.E., Thorley-Lawson D.A.;
RT "Molecular cloning of the lymphocyte activation marker Blast-1";
RL EMBO J. 6:3695-3701(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Bates K.;
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
TC TISSUE=B-cell;
RX MEDLINE-2238257; PubMed-12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield I.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE-91141511; PubMed-1847502;
RA Fisher R.C., Thorley-Lawson D.A.;
RT "Characterization of the Epstein-Barr virus-inducible gene encoding
RT the human leukocyte adhesion and activation antigen BLAST-1 (CD48).";
RL Mol. Cell. Biol. 11:1614-1623(1991).
RN [7]
RP PARTIAL SEQUENCE.
RX MEDLINE-91237281; PubMed-1827826;

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.
 JM protein - protein search, using sw model
 Run on: October 7, 2003, 11:09:22 ; Search time 96 seconds
 (without alignments)
 247.300 Million cell updates/sec

Title: US-09-730-465-2_COPY_1_92

Perfect score: 475
 Sequence: 1 MVAGSDAGRALGVLSVCLL.....AFSFKNRVYLDTVSGSLTI 92

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
 1: sp.archaea:*
 2: sp.bacteria:*
 3: sp.fungi:*
 4: sp.human:*
 5: sp.invertebrate:*
 6: sp.mammal:*
 7: sp.mhc:*
 8: sp.organelle:*
 9: sp.phage:*
 10: sp.plant:*
 11: sp.podent:*
 12: sp.virus:*
 13: sp.vertebrate:*
 14: sp.unclassified:*
 15: sp.rvirus:*
 16: sp.bacteriaph:*
 17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475	100.0	240	4 Q9BRW0	Q9brw0 homo sapien
2	328	69.1	134	4 Q14748	Q14748 homo sapien
3	287	60.4	119	4 Q16393	Q16393 homo sapien
4	256.5	54.0	159	6 Q28752	Q28752 ovis sp. lf
5	256.5	54.0	227	6 Q28754	Q28754 ovis sp. lf
6	256.5	54.0	253	6 Q28753	Q28753 ovis sp. lf
7	137.5	33.2	244	6 Q8SQB6	Q8sqb6 sus scrofa
8	122	25.7	357	13 Q90ZL5	Q90zls anas platyr
9	76	16.0	108	2 Q8GN34	Q8gn34 uncultured
10	75.5	15.9	1225	2 Q8GAT8	Q8gat8 altercomonas
11	74.5	15.7	169	7 Q8MGRO	Q8mgr0 homo sapien
12	73	15.4	928	5 Q8LIN2	Q8lin2 plasmodium
13	70	14.7	288	6 Q77684	Q77684 macaca mune
14	70	14.7	288	6 Q28499	Q28499 macaca mulia
15	70	14.7	288	6 Q902P8	Q902p8 caenorhabdi
16	69.5	14.6	389	5 Q20272	Q20272 caenorhabdi

17	68	14.3	499	3 Q9US44	Q9us44 schizosacch
18	67.5	14.2	499	5 Q9GP65	Q9gp65 trypanosoma
19	67.5	14.2	499	5 Q9GU80	Q9gu80 trypanosoma
20	67.5	14.2	946	11 Q9IY12	Q9iy12 mus musculu
21	67	14.1	200	12 Q9IW07	Q9iw07 poinsettia
22	67	14.1	1987	12 Q9IW08	Q9iw08 poinsettia
23	66.5	14.0	151	11 Q8C2T1	Q8c2t1 mus musculu
24	66.5	14.0	901	11 Q88191	Q88191 mus musculu
25	66.5	14.0	937	11 Q91Y13	Q91y13 mus musculu
26	66	13.9	661	12 Q8QM64	Q8qm64 ectocarpus
27	66	13.9	707	11 Q9ESI6	Q9esy6 rattus norv
28	65	13.7	341	5 Q9IXY7	Q9ixy7 plasmodium
29	65	13.7	416	5 Q18094	Q18094 caenorhabdi
30	64.5	13.6	174	2 Q8L344	Q8l344 vibrio chol
31	64.5	13.6	701	5 Q8IK93	Q8ik93 plasmodium
32	64	13.5	416	5 Q9N507	Q9n507 caenorhabdi
33	64	13.5	737	8 Q32744	Q32744 osteospermu
34	64	13.5	1293	10 Q9M8Z0	Q9m8z0 arabidopsis
35	63.5	13.4	340	11 Q9CXD6	Q9cxd6 mus musculu
36	63.5	13.4	505	5 Q8IDX5	Q8idx5 plasmodium
37	63.5	13.4	562	16 Q9KYG2	Q9kyg2 vibrio chol
38	63.5	13.4	612	16 Q8D3J0	Q8d3j0 wigglewort
39	63.5	13.4	781	16 Q8ERN0	Q8ewn0 mycoplasma
40	63.5	13.4	1126	16 Q9NS6	Q9ns6 rhizobium 1
41	63.5	13.4	1394	2 Q9AIU3	Q9aiu3 anaplasma p
42	63	13.3	290	9 Q8HA77	Q8ha77 bacterioph
43	63	13.3	294	16 Q92B18	Q92b18 listeria in
44	63	13.3	299	17 Q980R7	Q980r7 sulfolobus
45	63	13.3	334	5 Q8ILY8	Q8ily8 plasmodium

ALIGNMENTS

RESULT 1

Q9BRW0 PRELIMINARY; PRT; 240 AA.
 AC Q9BRW0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Similar to CD58 antigen, (Lymphocyte function-associated antigen 3).
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005930; AAH05930.1; -
 DR HSP; PI9256; ICCZ.
 DR InterPro: IPR003599; Ig.
 DR SMART; SM00409; IG; 1.
 SQ SEQUENCE 240 AA; 27044 MW; 431E44EFDDF80E2 CRC64;

Query Match 100.0%; Score 475; DB 4; Length 240;
 Best Local Similarity 100.0%; Pred. No. 1.8e-46;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVAGSDAGRALGVLSVCLLHCFGFCISCFQQIYGVYGVNTHFVSPNPLKYLKKOK 60
 Db 1 MVAGSDAGRALGVLSVCLLHCFGFCISCFQQIYGVYGVNTHFVSPNPLKYLKKOK 60
 QY 61 DKVAELENSEFRATSSFKNRVYLDTVSGSLTI 92
 Db 61 DKVAELENSEFRATSSFKNRVYLDTVSGSLTI 92

RESULT 2

Q14748


```
D Q14748 PRELIMINARY; PRT; 134 AA.
C Q14748;
T 01-NOV-1996 (TReMBLrel. 01, Created)
T 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
T 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
E LFA-3(delta D2) (Fragment).
S Homo sapiens (Human).
X Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
X Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
X [1]
X SEQUENCE FROM N.A.
X Kakutani T.;
X Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
X EMBL; D28586; BAA05922.1; -.
X HSSP; P19256; ICCZ.
X InterPro; IPR003599; Ig.
X SMART; SM00409; IG; 1.
X NON_TER 1
X SEQUENCE 134 AA; 15452 MW; 79BEF0A4EEB4E59B CRC64;

Query Match 69.1%; Score 328; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 7.5e-30;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 FSQIYGVVGNVTFHVPNSVPLKEVLKKQDKVAELENSEFRFSSFKNRVYLDTVSG 88
D 1 FSQIYGVVGNVTFHVPNSVPLKEVLKKQDKVAELENSEFRFSSFKNRVYLDTVSG 60
D 89 SLTI 92
D 61 SLTI 64

RESULT 3
Q16393 PRELIMINARY; PRT; 119 AA.
ID Q16393
AC Q16393;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE LFA-3 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
OX [1]
OX SEQUENCE FROM N.A.
OX MEDLINE=95398636; PubMed=7545392;
OX Kirby A.C., Hill V., Olsen I., Porter S.R.;
OX "LFA-3 delta D2: a novel in vivo isoform of lymphocyte function-
OX associated antigen 3.";
OX Biochem. Biophys. Res. Commun. 214:200-205(1995).
DR EMBL; S79616; AAB40000.2; -.
DR HSSP; P19256; ICCZ.
DR NON_TER 1
DR NON_TER 119
DR SEQUENCE 119 AA; 13732 MW; 4096AC6P45181505 CRC64;

Query Match 60.4%; Score 287; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.4e-25;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 YVGNVTFHVPNSVPLKEVLKKQDKVAELENSEFRFSSFKNRVYLDTVSGSLTI 92
D 1 YVGNVTFHVPNSVPLKEVLKKQDKVAELENSEFRFSSFKNRVYLDTVSGSLTI 56

RESULT 4
Q28752 PRELIMINARY; PRT; 159 AA.
ID Q28752
AC Q28752;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
```

```
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE LFA-3(delta D2) precursor.
OS Ovis sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9939;
OX [1]
OX SEQUENCE FROM N.A.
OX Kakutani T.;
OX Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
OX EMBL; D28583; BAA05919.1; -.
OX HSSP; P19256; ICCZ.
OX InterPro; IPR003599; Ig.
OX SMART; SM00409; IG; 1.
OX SIGNAL 1 28
OX SIGNAL 1 28
OX SEQUENCE 159 AA; 17645 MW; 592A97046ECD985E CRC64;

Query Match 54.0%; Score 256.5; DB 6; Length 159;
Best Local Similarity 58.1%; Pred. No. 1.5e-21;
Matches 54; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

QY 1 MVAGSDAGRALGYLVSVVCLLHCGFISCFSCFQQIYGVVGNVTFHVPNSVPLKEVLKKQK 60
D 1 MAAGSAPGCALGALGLVCLFLKLDIFISCVSQDIYGAMNGNVTFYVSESQPTTEIMWKKGK 60
QY 61 DKVAEL-ENSEFRFSSFKNRVYLDTVSGSLTI 92
D 61 DKVWMDQTSGLFAFQSFKNRVHLDIVSGNLTI 93

RESULT 5
Q28754 PRELIMINARY; PRT; 227 AA.
ID Q28754
AC Q28754;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE LFA-3(delta TM) precursor.
OS Ovis sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9939;
OX [1]
OX SEQUENCE FROM N.A.
OX Kakutani T.;
OX Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
OX EMBL; D28585; BAA05921.1; -.
OX HSSP; P19256; ICCZ.
OX InterPro; IPR003599; Ig.
OX SMART; SM00409; IG; 1.
OX SIGNAL 1 28
OX SIGNAL 29 227
OX CHAIN LFA-3(DELTA TM).
OX SEQUENCE 227 AA; 24760 MW; 1521A80CB49E9B55 CRC64;

Query Match 54.0%; Score 256.5; DB 6; Length 227;
Best Local Similarity 58.1%; Pred. No. 2.3e-21;
Matches 54; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

QY 1 MVAGSDAGRALGYLVSVVCLLHCGFISCFSCFQQIYGVVGNVTFHVPNSVPLKEVLKKQK 60
D 1 MAAGSAPGCALGALGLVCLFLKLDIFISCVSQDIYGAMNGNVTFYVSESQPTTEIMWKKGK 60
QY 61 DKVAEL-ENSEFRFSSFKNRVYLDTVSGSLTI 92
D 61 DKVWMDQTSGLFAFQSFKNRVHLDIVSGNLTI 93

RESULT 6
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 11:15:32 ; Search time 29 Seconds
(without alignments)
134.228 Million cell updates/sec

Title: US-09-730-465-2_COPY_1_92

Perfect score: 475

Sequence: 1 NVAGSDAGRALGVLSVVCLL.....AFSSFKRVYLDTVSGSLTI 92

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*

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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	475	100.0	240	1	US-07-940-861-12
2	475	100.0	240	1	US-08-459-512-12
3	475	100.0	240	2	US-08-459-657-12
4	475	100.0	240	2	US-08-460-132-12
5	475	100.0	240	3	US-08-466-465-4
6	475	100.0	240	5	PCT-US92-02050-12
7	475	100.0	240	6	5185441-36
8	475	100.0	240	6	5223394-4
9	475	100.0	240	6	5223394-6
10	475	100.0	250	1	US-07-940-861-10
11	475	100.0	250	1	US-08-459-512-10
12	475	100.0	250	2	US-08-459-657-10
13	475	100.0	250	2	US-08-460-132-10
14	475	100.0	250	3	US-08-466-465-2
15	475	100.0	250	5	PCT-US92-02050-10
16	475	100.0	250	6	5223394-1
17	475	100.0	251	6	5185441-38
18	475	100.0	347	1	US-07-940-861-43
19	475	100.0	347	1	US-08-459-512-43
20	475	100.0	347	1	US-08-459-657-43
21	475	100.0	347	2	US-08-460-132-43
22	475	100.0	347	3	US-08-466-465-8
23	475	100.0	347	5	PCT-US92-02050-43
24	402	84.6	77	1	US-07-940-861-5
25	402	84.6	77	1	US-08-459-512-5
26	402	84.6	77	2	US-08-459-657-5
27	402	84.6	77	2	US-08-460-132-5

28 402 84.6 77 5 PCT-US92-02050-5
29 328 69.1 134 1 US-08-328-152A-13
30 328 69.1 222 1 US-08-328-152A-8
31 260 54.7 50 1 US-07-940-861-2
32 260 54.7 50 1 US-08-459-512-2
33 260 54.7 50 2 US-08-459-657-2
34 260 54.7 50 2 US-08-460-132-2
35 260 54.7 50 5 PCT-US92-02050-2
36 200 42.1 38 6 5185441-1
37 186.5 39.3 131 1 US-08-328-152A-1
38 186.5 39.3 199 1 US-08-328-152A-36
39 186.5 39.3 225 1 US-08-328-152A-31
40 74.5 15.7 194 3 US-08-630-172-14
41 74.5 15.7 194 3 US-09-375-419-14
42 73 15.4 16 1 US-07-940-861-7
43 73 15.4 16 1 US-08-459-512-7
44 73 15.4 16 2 US-08-459-657-7
45 73 15.4 16 2 US-08-460-132-7

ALIGNMENTS

RESULT 1
US-07-940-861-12
; Sequence 12, Application US/07940861
; Patent No. 5547853
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALINER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-8250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,861
; FILING DATE: 21-OCT-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Sequence 5, Appli
Sequence 13, Appli
Sequence 8, Appli
Sequence 2, Appli
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Sequence 2, Appli
Patent No. 5185441
Sequence 1, Appli
Sequence 36, Appli
Sequence 31, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli

MOLECULE TYPE: protein

JS-07-940-861-12

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Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MVAGSDAGRALGVLSVYVCLLHCFGFCFSCFSQQIYGVYGNVTFHVPNSVPLKEVLWKOK 60

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Db 61 DKVAELENSEFRAPSSFKNRVYLDTVSGSLTI 92

RESULT 2

US-08-459-512-12

; Sequence 12, Application US/08459512

; Patent No. 5728677

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; APPLICANT: WALLNER, Barbara P.

; APPLICANT: MILLER, Glenn T.

; APPLICANT: ROSA, Margaret D.

; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 875 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022-6250

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,512

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02050

; FILING DATE: 12-MAR-1992

; APPLICATION NUMBER: US 07/667,971

; FILING DATE: 12-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/770,967

; FILING DATE: 07-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: HALEY, James F., Jr.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: B151CIP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)715-0600

; TELEFAX: (212)715-0673

; TELEX: 14-8367

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 240 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-459-512-12

Query Match

Best Local Similarity 100.0%;

Pred. No. 1.1e-51;

Matches 92; Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

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Db 1 MVAGSDAGRALGVLSVYVCLLHCFGFCFSCFSQQIYGVYGNVTFHVPNSVPLKEVLWKOK 60

QY 61 DKVAELENSEFRAPSSFKNRVYLDTVSGSLTI 92

Db 61 DKVAELENSEFRAPSSFKNRVYLDTVSGSLTI 92

RESULT 3

US-08-459-657-12

; Sequence 12, Application US/08459657

; Patent No. 5914111

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; APPLICANT: WALLNER, Barbara P.

; APPLICANT: MILLER, Glenn T.

; APPLICANT: ROSA, Margaret D.

; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 875 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022-6250

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,657

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02050

; FILING DATE: 12-MAR-1992

; APPLICATION NUMBER: US 07/667,971

; FILING DATE: 12-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/770,967

; FILING DATE: 07-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: HALEY, James F., Jr.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: B151CIP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)715-0600

; TELEFAX: (212)715-0673

; TELEX: 14-8367

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 240 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-459-657-12

Query Match

Best Local Similarity 100.0%;

Pred. No. 1.1e-51;

Matches 92; Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

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QY 61 DKVAELENSEFRAPSSFKNRVYLDTVSGSLTI 92

Db 61 DKVAELENSEFRAPSSFKNRVYLDTVSGSLTI 92

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 11:17:27 ; Search time 67 seconds
(without alignments)
217.248 Million cell updates/sec

Title: US-09-730-465-2_COPY_1_92

Perfect score: 475
Sequence: 1 MVAGSDAGRALGVLSVWCLL.....AFSFKNRVYLDIVSGSLTI 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 segs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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11	475	100.0	347	15	US-10-091-268-7
12	74.5	15.7	96	9	US-09-864-761-47502
13	74.5	15.7	243	11	US-09-860-836B-13
14	74.5	15.7	243	12	US-10-436-523-62
15	74.5	15.7	243	15	US-10-207-655-111

16	71	14.9	287	12	US-10-032-214-237	Sequence 237, App
17	70	14.7	288	12	US-10-032-214-72	Sequence 72, Appl
18	70	14.7	288	12	US-10-032-214-82	Sequence 82, Appl
19	70	14.7	288	12	US-10-032-214-83	Sequence 83, Appl
20	70	14.7	288	12	US-10-032-214-93	Sequence 227, App
21	70	14.7	288	12	US-10-032-214-221	Sequence 246, App
22	70	14.7	288	12	US-10-032-214-246	Sequence 251, App
23	70	14.7	288	12	US-10-032-214-251	Sequence 252, App
24	70	14.7	288	12	US-10-032-214-252	Sequence 252, App
25	70	14.7	288	12	US-10-032-214-279	Sequence 279, App
26	68	14.3	287	12	US-10-032-214-74	Sequence 74, Appl
27	68	14.3	288	12	US-10-032-214-75	Sequence 75, Appl
28	68	14.3	288	12	US-10-032-214-77	Sequence 77, Appl
29	68	14.3	288	12	US-10-032-214-78	Sequence 78, Appl
30	68	14.3	288	12	US-10-032-214-87	Sequence 87, Appl
31	68	14.3	288	12	US-10-032-214-91	Sequence 91, Appl
32	68	14.3	288	12	US-10-032-214-92	Sequence 92, Appl
33	68	14.3	288	12	US-10-032-214-234	Sequence 234, App
34	68	14.3	288	12	US-10-032-214-247	Sequence 247, App
35	68	14.3	288	12	US-10-032-214-286	Sequence 286, App
36	67.5	14.2	240	11	US-09-860-836B-15	Sequence 15, Appl
37	67	14.1	288	12	US-10-032-214-85	Sequence 85, Appl
38	67	14.1	288	12	US-10-032-214-88	Sequence 88, Appl
39	67	14.1	288	12	US-10-032-214-289	Sequence 289, App
40	66	13.9	288	12	US-10-032-214-287	Sequence 287, App
41	66	13.9	707	12	US-09-354-342-43	Sequence 43, Appl
42	65	13.7	288	12	US-10-032-214-288	Sequence 288, App
43	64	13.5	288	12	US-10-032-214-235	Sequence 235, App
44	63.5	13.4	351	11	US-09-829-275-2	Sequence 2, Appl
45	63	13.3	287	12	US-10-032-214-243	Sequence 243, App

ALIGNMENTS

RESULT 1

US-09-796-033-4
; Sequence 4, Application US/09796033
; Patent No. US20020009446A1
; GENERAL INFORMATION:
; APPLICANT: Magilavay, Daniel
; TITLE OF INVENTION: METHOD OF MODULATING MEMORY EFFECTOR
; FILE OF INVENTION: T-CELLS AND COMPOSITIONS
; FILE REFERENCE: 10274-044001
; CURRENT APPLICATION NUMBER: US/09/796.033
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: PCT/US99/20026
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 60/098,456
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-09-796-033-4

Query Match 100.0%; Score 475; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 1,7e-49;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAGSDAGRALGVLSVWCLLHCFGFCISFCSQIYGVYGVNTHVPSNVLKVLKKOK 60

DB 1 MVAGSDAGRALGVLSVWCLLHCFGFCISFCSQIYGVYGVNTHVPSNVLKVLKKOK 60

QY 61 DKVAELENSEFRASFKNRVYLDIVSGSLTI 92

DB 61 DKVAELENSEFRASFKNRVYLDIVSGSLTI 92

RESULT 2

S-09-730-465-4

Sequence 4, Application US/09730465

Patent No. US2002009449A1

GENERAL INFORMATION:

APPLICANT: Wallner, Barbara P.

Cooper, Kevin D.

TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
Presenting Cell Driven Skin Conditions Using

Inhibitors of the CD2/LFA-3 Interaction

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 05-Dec-2000

APPLICATION NUMBER: US/09/730,465

PRIOR APPLICATION DATA:

FILING DATE: 06-Oct-1992

APPLICATION NUMBER: PCT/US92/08755

FILING DATE: 12-APR-1992

APPLICATION NUMBER: US 07/862,022

FILING DATE: 07-OCT-1991

APPLICATION NUMBER: US 07/770,969

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis (PLM)

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: BGP-111CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-730-465-4

Query Match

Best Local Similarity 100.0%; Score 475; DB 9; Length 240;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MVAGSDAGRALGVLSVCLLHCFGFCISCSQIYGVVGNVTFHVPSPNPLKEVLKKQK 60

QY 61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTI 92

DB 61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTI 92

RESULT 3

US-09-796-033-2

Sequence 2, Application US/09796033

Patent No. US2002009446A1

GENERAL INFORMATION:

APPLICANT: Magilavy, Daniel

TITLE OF INVENTION: METHOD OF MODULATING MEMORY EFFECTOR

TITLE OF INVENTION: T-CELLS AND COMPOSITIONS

FILE REFERENCE: 10274-044001

CURRENT APPLICATION NUMBER: US/09/796,033

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: PCT/US99/20026

PRIOR FILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: US 60/098,456

PRIOR FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 250

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)...(28)

US-09-796-033-2

Query Match

Best Local Similarity 100.0%; Score 475; DB 9; Length 250;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DKVAELENSEFRAFSSFKNRVYLDTVSGSLTI 92

RESULT 4

US-09-730-465-2

Sequence 2, Application US/09730465

Patent No. US2002009449A1

GENERAL INFORMATION:

APPLICANT: Wallner, Barbara P.

Cooper, Kevin D.

TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
Presenting Cell Driven Skin Conditions Using

Inhibitors of the CD2/LFA-3 Interaction

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/730,465

FILING DATE: 05-Dec-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/08755

FILING DATE: 06-Oct-1992

APPLICATION NUMBER: US 07/862,022

FILING DATE: 12-APR-1992

APPLICATION NUMBER: US 07/770,969

FILING DATE: 07-Oct-1991

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis (PLM)

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: BGP-111CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 250 amino acids

TYPE: amino acid

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

AM protein - protein search, using sw model

Run on: October 7, 2003, 16:34:43 ; Search time 17.9412 Seconds
(without alignments)
539.670 Million cell updates/sec

Title: US-09-730-465-2_COPY_20_80

Perfect score: 327

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_13Jun03.*

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1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
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19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	112	23 ABB81992	Human transmembran
2	327	100.0	120	13 AAR27157	LFA-3 CD2 binding
3	327	100.0	128	17 AAW04361	Human cell adhesio
4	327	100.0	133	17 AAW04362	Human cell adhesio
5	327	100.0	133	17 AAW04363	Human cell adhesio
6	327	100.0	237	12 AAR14182	Human LFA-3(CD58)
7	327	100.0	237	13 AAR20804	Human LFA-3 antige
8	327	100.0	237	17 AAR91432	Human LFA-3 antige
9	327	100.0	237	19 AAW80441	Human LFA-3 antige

10	327	100.0	237	20 AAW86189	Human LFA-3 antige
11	327	100.0	237	21 AAY96127	Human cell surface
12	327	100.0	237	22 AAU02436	Human lymphocyte f
13	327	100.0	240	11 AAR05572	PI-linked LFA-3 en
14	327	100.0	240	11 AAR07604	Lymphocyte functio
15	327	100.0	240	13 AAR27162	PI-linked LFA-3 us
16	327	100.0	240	14 AAR34372	Sequence encoded b
17	327	100.0	240	21 AAY83134	PI-linked human tr
18	327	100.0	240	22 AAB61158	Human PI-linked tr
19	327	100.0	240	23 AAU76226	PI-linked lymphocy
20	327	100.0	250	9 AAP91507	Human LFA-3 expres
21	327	100.0	250	13 AAR27161	transmembrane LFA-
22	327	100.0	250	14 AAR34371	Sequence encoded b
23	327	100.0	250	15 AAR64271	Human LFA-3. Homo
24	327	100.0	250	17 AAW04370	Human cell adhesio
25	327	100.0	250	21 AAY83133	Human transmembran
26	327	100.0	250	22 AAB61157	Human transmembran
27	327	100.0	250	23 AAU76225	Lymphocyte functio
28	327	100.0	256	24 AA016017	Murine CD2-binding
29	327	100.0	280	22 AAG18595	Novel human diagno
30	327	100.0	347	13 AAR27163	CD2 binding LFA-3-
31	327	100.0	347	21 AAY83136	Human transmembran
32	327	100.0	347	22 AAB61160	Human LFA3TIP fusi
33	327	100.0	347	23 AAG70766	Human lymphocyte f
34	327	100.0	347	23 ABB81994	Human LFA3TIP poly
35	327	100.0	347	23 AAU76328	LFA3/IgG fusion pr
36	327	100.0	347	24 ABP58178	Murine LFA-3. Mus
37	327	100.0	351	23 ABB81995	Human LFA-3/IgG fu
38	324	99.1	240	14 AAR34222	Amino acid sequenc
39	324	99.1	250	14 AAR34221	Amino acid sequenc
40	321	98.2	237	18 AAW16687	Human CD58 GPI. H
41	319	97.6	347	14 AAR34224	Amino acid sequenc
42	317	96.9	250	13 AAR28365	Human LFA-3 protei
43	271	82.9	71	13 AAR27158	LFA-3 CD2 binding
44	271	82.9	134	13 AAR28364	Human LFA-3 D2 reg
45	271	82.9	135	13 AAR28369	Human LFA-3-delca-

ALIGNMENTS

RESULT 1
ABB81992
ID ABB81992 standard; Protein; 112 AA.
XX AC ABB81992;
XX DT 25-NOV-2002 (first entry)
XX DE Human transmembrane LFA-3 partial polypeptide.

XX DE Human; immunosuppressive; antithyroid; dermatological; antiinflammatory;
KW antipsoriatic; antirheumatic; antiarthritic; neuroprotective; vaccine;
KW osteopathic; antidiabetic; gene therapy; CD2; LFA-3; interferon; IFN;
KW CD25; CD8; CD45.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Peptide 1..28 /note= "signal peptide"

FT Protein 29..84

FT /note= "partial mature protein fragment; the sequence after position 84 is not indicated in the specification; the pages containing the complete sequence are not provided"

WO200260480-A1.

08-AUG-2002.

25-JAN-2002; 2002WO-US02314.

XX

XX	12-MAR-1992;	92EP-0104320.
XX	PF	
XX	PR	9IUS-0667971.
XX	PR	9IUS-0770967.
XX	(BIOJ)	BIOGEN INC.
XX	PA	
XX	PI	
XX	DR	Miller GT, Rosa MD, Wallner BP;
XX	DR	WPI; 1992-309760/38.
XX	DR	
XX	PT	CD2-binding domain of lymphocyte function associated antigen-3
XX	PT	and DNA - for diagnosing and treating inflammation and
XX	PT	auto-immune diseases, e.g. systemic lupus erythematosus and
XX	PT	rheumatoid arthritis
XX	PS	Claim 1; Page 52-53; 85pp; English.
XX	XX	
CC	This polypeptide can bind to CD2. The N-terminal Met is opt.	
CC	absent. The N-terminal and C-terminal portions can be deleted.	
CC	The polypeptide and its functional deletion mutants may be used to	
CC	treat acute and chronic inflammation, autoimmune disease and for	
CC	immunomodulation. The polypeptides can also form the N-terminal	
CC	part of a fusion protein. The polypeptides and fusion proteins may	
CC	also be used to inhibit T-cell activation and the proliferation of	
CC	peripheral blood lymphocytes. Multimeric proteins can be formed from	
CC	the polypeptides and/or fusion proteins. The multimers have enhanced	
CC	affinity for CD2. See also AAR27157-9.	
CC	(Updated on 25-MAR-2003 to correct PN field.)	
XX	SQ	Sequence 120 AA:
XX	Query Watch	100.0%; Score 327; DB 13; Length 120;
XX	Best Local Similarity	100.0%; Pred. No. 2.4e-34;
XX	Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 LHCFCGFISCFQQIYGVGIVGNVTFHVPNSNPLKEVLWKKOKDKVAELENSEFRAFSSFKN 60	
Db	20 LHCFCGFISCFQQIYGVGIVGNVTFHVPNSNPLKEVLWKKOKDKVAELENSEFRAFSSFKN 79	
QY	61 R 61	
Db		
Db	80 R 80	
RESULT 3		
AARW04361		
ID	AAW04361 standard; Protein; 128 AA.	
AC	AAW04361;	
DT	27-JUN-1997 (first entry)	
DE	Human cell adhesion protein LFA-3.	
KW	Human; T cell; MOLT-4; cell adhesion; LFA-3; immunosuppression;	
XX	cell line; immunosuppressant cell.	
OS	Homo sapiens.	
PN	WO9633217-A1.	
PD	24-OCT-1996.	
PF	15-APR-1996; 96WO-JP01039.	
XX	27-DEC-1995; 95JP-0341959.	
PR	19-APR-1995; 95JP-0094060.	
XX	04-JUL-1995; 95JP-0169110.	
XX	(KANF) KANEGAFUCHI KAGAKU KOGYO KK.	
XX		

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XM protein - protein search, using sw model

run on: October 7, 2003, 16:45:48 ; Search time 7.47549 Seconds
(without alignments)
784.736 Million cell updates/sec

Title: US-09-730-465-2_COPY_20_80

Perfect score: 327

Sequence: 1 LHCFGFISCFQQIYGVYVG.....DKVAELENSEFRASFKNR 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	250	2	A28564 lymphocyte functio
2	67	20.5	546	2	T26568 hypothetical prote
3	63.5	19.4	562	2	C82355 hypothetical prote
4	62	19.0	416	2	T25036 hypothetical prote
5	60.5	18.5	275	2	E83655 signal peptidase-1
6	60.5	18.5	508	1	A30007 dolichyl-diphospho
7	60.5	18.5	1822	2	S44849 K12H4.8 protein -
8	60.5	18.5	2924	2	T18378 variant-specific s
9	60	18.3	405	2	S41917 methionine adenosy
10	60	18.3	619	2	C96714 unknown protein t6
11	60	18.3	852	2	A00050 probable phosphoen
12	59.5	18.2	273	2	B64608 outer membrane pro
13	59	18.0	294	2	ADL649 weakly phase relat
14	59	18.0	344	2	T00993 probable beta-1,3-
15	59	18.0	475	2	T12955 probable protein k
16	59	18.0	511	2	B81332 GMP synthase (glut
17	58.5	17.9	508	2	F71865 GMP synthetase - H
18	58.5	17.9	656	2	S34197 DNA-binding protei
19	58	17.7	237	2	C70157 hypothetical prote
20	58	17.7	299	2	E90162 conserved hypothe
21	58	17.7	679	2	S54299 transketolase (EC
22	58	17.7	719	2	D90083 probable helicase-
23	58	17.7	737	2	T13504 NADH2 dehydrogenas
24	57.5	17.6	401	2	E69501 sugar transporter
25	57.5	17.6	425	2	T24111 hypothetical prote
26	57.5	17.6	632	2	C81261 transketolase (EC
27	57.5	17.6	786	2	AG2375 WD-40 repeat-prote
28	57.5	17.6	1157	2	T40572 protein phosphatas
29	57	17.4	509	2	D86146 F22L4.11 protein -

30 56.5 17.3 299 2 D81871 RdcG protein NMA10
31 56.5 17.3 299 2 F81149 recombination asso
32 56.5 17.3 1656 2 S54520 probable membrane
33 56 17.1 142 2 E71079 hypothetical prote
34 56 17.1 265 2 G75067 hypothetical prote
35 56 17.1 274 2 S76154 hypothetical prote
36 56 17.1 378 2 G96630 omega-6 fatty acid
37 56 17.1 382 2 T15042 probable enoyl-CoA
38 56 17.1 601 2 T38200 spliceosome associ
39 56 17.1 745 2 S57048 hypothetical prote
40 56 17.1 752 2 H97191 uncharacterized pr
41 56 17.1 918 2 C84720 hypothetical prote
42 56 17.1 1107 1 S52517 myosin I heavy cha
43 56 17.1 1363 2 T43220 insulin-like growt
44 55.5 17.0 348 2 B64552 conserved hypothet
45 55.5 17.0 351 2 D71955 hypothetical prote

ALIGNMENTS

RESULT 1

A28564
lymphocyte function-associated antigen 3, transmembrane splice form precursor - hum
N:Alternate names: CD58 antigen; surface glycoprotein LFA-3
C:Species: Homo sapiens (man)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 02-Aug-2002
C:Accession: A28564; S01269
R:Wallner, B.P.; Frey, A.Z.; Tizard, R.; Mattaliano, R.J.; Hession, C.; Sanders, M.
J. Exp. Med. 166, 923-932, 1987
A:Title: Primary structure of lymphocyte function-associated antigen 3 (LFA-3). The
A:Reference number: A28564; MUID:88009714; PMID:3309127
A:Accession: A28564
A:Molecule type: mRNA
A:Residues: 1-250 <WAL>
A:CROSS-references: DB:Y00636; NID:g34346; PIDN:CAA68668.1; PID:g34347
A:Experimental source: erythrocytes
A>Note: the authors translated the codon TAT for residue 34 as Val
R:Seed, B.
Nature 329, 840-842, 1987
A:Title: An LFA-3 cDNA encodes a phospholipid-linked membrane protein homologous to
A:Reference number: S01269; MUID:88039074; PMID:3313052
A:Accession: S01269
A:Molecule type: mRNA
A:Residues: 1-235, 'VL' <SEE>
A:CROSS-references: EMBL:X06296; NID:g34349; PIDN:CAA29622.1; PID:g34350
C:Comment: For an alternative splice form, see PIR:S01269.
C:Comment: For an alternative splice form, see PIR:A28564.
C:Genetics:
A:Gene: GDB:CD58; LFA3
A:CROSS-references: GDB:120580; OMIM:153420
A:Map position: lp13-lp13
C:Superfamily: human B-cell antigen CD19; immunoglobulin homology
F:1-30/Domain: alternative splicing; glycoprotein; phosphatidylinositol linkage; surfa
F:31-250/Product: lymphocyte function-associated antigen 3 transmembrane splice for
F:135-189/Domain: immunoglobulin homology <LMM>
F:40,94,109,135,169,195/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 100.0%; Score 327; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.1e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHCFGFISCFQQIYGVYGVYGVNTPFVSNVPLKVLWKQDKVAELENSEFRASFKNR 60

DB 20 LHCFGFISCFQQIYGVYGVYGVNTPFVSNVPLKVLWKQDKVAELENSEFRASFKNR 79

QY 61 R 61

DB 80 R 80

RESULT 2

A:Molecule type: DNA
A:Residues: 1-416 <WIL>
A:Cross-references: EMBL:Z81594; PIDN:CA04746.1; GSPDB:GN00019; CESP:T20F10.4
A:Experimental source: clone T20F10
C:Genetics:
A:Gene: CESP:T20F10.4
A:Map position: 1

Query Match 19.0%; Score 62; DB 2; Length 416;
Best Local Similarity 35.7%; Pred. No. 13;
Matches 10; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 2 HCFGFIQSQIIYGVIYGVNTVTPSN 29
| | | | : | : | : | : | : |
Db 165 HIFGEVCYNKIYGRKHNLSLYRSPEN 192

RESULT 5
E83655
signal peptidase-like protein BH0045 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: E83655
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A:title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83655
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <STO>
A:Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03764.1; GSPDB
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0045
C:Superfamily: probable signal peptidase II yaat

Query Match 18.5%; Score 60.5; DB 2; Length 275;
Best Local Similarity 44.2%; Pred. No. 12;
Matches 19; Conservative 5; Mismatches 12; Indels 7; Gaps 3;

QY 16 GVTVGNVTFT---VPST--VPLKEVL-WKKOKDKVALENSE 51
| | | | | | | | | | : | | | : | | | | | |
Db 38 GVEIGNVYIEKTVGDNDVLPKQIVRVATEKDGLAVQENKE 80

RESULT 6
A30007
dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) glycosylat
C:Species: Gallus gallus (chicken)
C>Date: 15-Dec-1988 #sequence_revision 26-May-1994 #text_change 03-Jun-2002
C:Accession: A30007
R:Geetha-Habib, M.; Noiva, R.; Kaplan, H.A.; Lennarz, W.J.
Cell 54, 1053-1060, 1988
A:title: Glycosylation site binding protein, a component of oligosaccharyl transferase
A:Reference number: A30007; MUID:883227849; PMID:2458190
A:Accession: A30007
A:Molecule type: mRNA
A:Residues: 1-508 <GEN>
C:Cross-references: EMBL:N22594
C:Superfamily: protein disulfide-isomerase; thioredoxin homology
C:Keywords: duplication; endoplasmic reticulum; glycosyltransferase; hexosyltransferase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-508/Product: dolichyl-diphosphooligosaccharide-protein glycotransferase glycosy
F:31-118/Domain: thioredoxin homology <rx1>
F:376-461/Domain: thioredoxin homology <rx2>
F:505-508/Region: endoplasmic reticulum retention signal
F:52-55,398-401/Disulfide bonds: redox-active #status predicted
F:312-343/Disulfide bonds: #status predicted

Query Match 18.5%; Score 60.5; DB 1; Length 508;
Best Local Similarity 43.9%; Pred. No. 24;
Matches 18; Conservative 3; Mismatches 19; Indels 1; Gaps 1;

GenCore version 5.1.6
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M protein - protein search, using sw model

run on: October 7, 2003, 16:35:28 ; Search time 4.03677 Seconds
(without alignments)
710.626 Million cell updates/sec

File: US-09-730-465-2_COPY_20_80

Perfect score: 327

Sequence: 1 LHCFGIFCSQGIYGVYG.....DKVAELENSEFRAGSFKNR 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	DB ID	Description
1	327	100.0	250	1 LPA3_HUMAN	P19256 homo sapien
2	61.5	18.8	379	1 ASPN_HUMAN	Q9bxi1 homo sapien
3	60.5	18.5	373	1 ASPN_MOUSE	Q99mq4 mus musculu
4	60.5	18.5	508	1 GSBP_CHICK	P12244 gallus gall
5	60	18.3	408	1 METK_DROME	P40320 drosophila
6	59	18.0	438	1 ARLY_CLOTE	P59616 clostridium
7	59	18.0	511	1 GUAA_CAMEL	Q9pn49 campylobact
8	58.5	17.9	508	1 GUAA_HELPJ	Q9zkg4 helicobacte
9	58	17.7	679	1 XTFA_CRAPL	Q42675 craterostig
10	57.5	17.6	552	1 YHLL_SCHPO	Q9c0w8 schizosacch
11	56.5	17.3	299	1 RDGC_NEIGO	O87408 neisseria g
12	56.5	17.3	299	1 RDGC_NEIMA	Q9jv02 neisseria m
13	56.5	17.3	299	1 RDGC_NEIMA	Q9jv02 neisseria m
14	56.5	17.3	974	1 ATXB_LEIDO	P12532 leishmania
15	56.5	17.3	1656	1 ATC8_YEAST	Q12674 saccharomyc
16	56	17.1	745	1 Y100_YEAST	P47101 saccharomyc
17	56	17.1	1107	1 MYLE_RAT	Q63356 rattus norv
18	56	17.1	1363	1 ILPR_BRALA	Q02466 branchiost
19	55.5	17.0	348	1 Y258_HELPJ	P56136 helicobacte
20	55.5	17.0	350	1 Y258_HELPJ	Q9znh8 helicobacte
21	55.5	17.0	974	1 C615_YEAST	P27636 saccharomyc
22	55	16.8	651	1 Y942_MERJA	O58352 methanococ
23	55	16.8	844	1 MELV_VARV	P33057 variola vir
24	55	16.8	950	1 ORPL_HUMAN	Q9bxx6 homo sapien
25	54.5	16.7	195	1 MOBA_YERPE	O8zjs4 yersinia pe
26	54.5	16.7	544	1 MLH1_HORVU	Q49873 hordeum vul
27	54.5	16.7	898	1 TOP1_SYNY3	P73810 synecocyst
28	54.5	16.7	974	1 ARXA_LEIDO	P11718 leishmania
29	54	16.5	833	1 PIJA_ECOLI	P32670 escherichia
30	54	16.5	1010	1 CONT_CHICK	P14781 gallus gall
31	54	16.5	1109	1 MYLE_HUMAN	Q12965 homo sapien
32	53.5	16.4	210	1 RL13_MOUSE	P47963 mus musculu
33	53.5	16.4	304	1 PAGO_SALTY	O30646 salmonella

ALIGNMENTS

RESULT 1

ID	LPA3_HUMAN	STANDARD;	PRT;	250 AA.
34	53.5	16.4	560	1 ASNS_RAT
35	53.5	16.4	681	1 TRE_MANSE
36	53.5	16.4	1118	1 YIPL_YEAST
37	53.5	16.4	1178	1 RPOB_MYCLE
38	53.5	16.4	1178	1 RPOB_MYCTU
39	53	16.2	212	1 SODF_STRCO
40	53	16.2	329	1 YX99_BACHD
41	53	16.2	340	1 VB17_VARV
42	53	16.2	368	1 PGS1_XENLA
43	53	16.2	474	1 CBLC_HUMAN
44	53	16.2	490	1 YAM7_SCHPO
45	53	16.2	526	1 SI7A_MOUSE
AC	P19256; Q96KI9;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Lymphocyte function-associated antigen 3 precursor (Ag3) (Antigen			
DE	CD58) (Surface glycoprotein LFA-3).			
GN	CD58 OR LFA3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.			
RC	TISSUE=Erythrocyte;			
RX	MEDLINE=88009714; PubMed=3309127;			
RA	Wallner B.P., Frey A.Z., Tizard R., Mattaliano R.J., Hession C.,			
RA	Sanders M.E., Dustin M.L., Springer T.A.;			
RT	"Primary structure of lymphocyte function-associated antigen 3 (LFA-			
RT	3). The ligand of the T lymphocyte CD2 glycoprotein.";			
RL	J. Exp. Med. 166:923-932(1987).			
[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=88039074; PubMed=3313052;			
RA	Seed B.;			
RT	"An LFA-3 cDNA encodes a phospholipid-linked membrane protein			
RL	homologous to its receptor CD2.";			
Nature	329:840-842(1987).			
[3]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
MEDLINE=98169008;	PubMed=9510189;			
RA	Wallich R., Brenner C., Brand Y., Roux M., Reister M., Meuer S.;			
RT	"Gene structure, promoter characterization, and basis for alternative			
RNA	splicing of the human CD58 gene.";			
J. Immunol.	160:2862-2871(1998).			
[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 29-122.			
RA	Ikemizu S., Sparks L.M., van der Merwe P.A., Harlos K., Stuart D.I.,			
Jones B.Y., Davis S.J.;				
RT	"Crystal structure of the CD2-binding domain of CD58 (lymphocyte			
function-associated antigen 3) at 1.8-A resolution.";				
Proc. Natl. Acad. Sci. U.S.A.	96:4289-4294(1999).			
CC	-!- FUNCTION: LIGAND OF THE T LYMPHOCYTE CD2 GLYCOPROTEIN. THIS			
INTERACTION IS IMPORTANT IN MEDIATING THYMOCYTE INTERACTIONS WITH				
THYMIC EPITHELIAL CELLS, ANTIGEN-INDEPENDENT AND -DEPENDENT				
INTERACTIONS OF T LYMPHOCYTES WITH TARGET CELLS AND ANTIGEN-				
PRESENTING CELLS AND THE T LYMPHOCYTE ROSETTING WITH ERYTHROCYTES.				
IN ADDITION, THE LFA-3/CD2 INTERACTION MAY PRIME RESPONSE BY BOTH				
THE CD2+ AND LFA-3+ CELLS.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and			
attached to the membrane by a GPI-anchor (isoform 2).				
CC	-!- ALTERNATIVE PRODUCTS:			
Event=Alternative splicing; Named isoforms=2;				

P49088 rattus norv
P22297 manduca sex
P40456 saccharomyc
P30760 mycobacteri
P47766 mycobacteri
O51917 streptomyc
Q9K7g2 bacillus ha
P33878 variola vir
Q9ib75 xenopus lae
Q9ulv8 homo sapien
Q10062 schizosach
Q9qz39 mus musculu

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	327	100.0	240	4	Q9BRW0	Q9brw0 homo sapien
2	82.9	134	4	Q14748	Q14748 homo sapien	
3	230	70.3	119	4	Q16393	Q16393 homo sapien
4	165.5	50.6	159	6	Q28752	Q28752 ovis sp. lf
5	165.5	50.6	227	6	Q28754	Q28754 ovis sp. lf
6	165.5	50.6	253	6	Q28753	Q28753 ovis sp. lf
7	111.5	34.1	244	6	Q8SQB6	Q8sqb6 sus scrofa
8	99	30.3	357	13	Q9OZL5	Q9ozl5 anas platyr
9	67	20.5	546	5	Q9U2P8	Q9u2p8 caenorhabdi
10	65	19.9	108	2	Q8GM34	Q8gm34 uncultured
11	63.5	19.4	562	16	Q9KVG2	Q9kvg2 vibrio chol
12	63	19.3	515	10	Q8S7S6	Q8s7s6 oryza sativ
13	62.5	18.1	413	5	Q8I333	Q8i333 plasmodium
14	62.5	19.1	749	5	Q8IEC9	Q8iec9 plasmodium
15	62	19.0	205	5	Q15795	Q15795 plasmodium
16	62	19.0	252	5	Q8IC03	Q8ic03 plasmodium


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[1]
RP SEQUENCE FROM N.A.
RA Kakutani T.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: D28584; BAA05920.1; -.
DR HSP: P19256; ICCZ.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR001993; Mitoch_carrier.
DR SMART: SM00409; IG; 1.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
KW SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 253 AA; 27715 MW; 4A4E97A38519B290 CRC64;

Query Match 50.6%; Score 165.5; DB 6; Length 253;
Best Local Similarity 57.9%; Pred. NO. 3.6e-12;
Matches 33; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 6 FTSFQQIYGVVYGNVTHFVPSNPLKVLWKOKDKVAEL-ENSERAFSSFKNR 61
DB 25 FISCVSQDIYAGNGNVIFVSEQSFTEIMWKKGDKVWEDQTSGLERAFQSFNR 81

RESULT 7
O8SQB6 PRELIMINARY; PRT; 244 AA.
AC O8SQB6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CD58 antigen.
GN CD58.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Brossay A., Hube F., Bardos P., Watier H.;
RT "Characterization of the porcine CD58 antigen mRNA sequence.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF469666; AAL76278.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR001993; Mitoch_carrier.
DR SMART: SM00409; IG; 1.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
SQ SEQUENCE 244 AA; 27301 MW; 164B81ACC7A512D2 CRC64;

Query Match 34.1%; Score 111.5; DB 6; Length 244;
Best Local Similarity 42.1%; Pred. NO. 1.4e-05;
Matches 24; Conservative 8; Mismatches 24; Indels 1; Gaps 1;

QY 6 FTSFQQIYGVVYGNVTHFVPSNPLKVLWKOKDKVAELNS-EFRATSSFKNR 61
DB 25 FHCDSKVIYGAHKVNTLRASSQTFQELIWKKGDKRAVEEQYNTATPPFVDR 81

RESULT 8
O90ZL5 PRELIMINARY; PRT; 357 AA.
AC O90ZL5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CD58 antigen.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8639;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-White Pekin;
RC Chan S.W.S., Middleton D.L., Lundqvist M., Warr G.W., Higgins D.A.;
RA
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RT "Anas platyrhynchos T cell antigens.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY032731; AAK51607.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 1.
SQ SEQUENCE 357 AA; 39930 MW; 274161DF83868C08 CRC64;

Query Match 30.3%; Score 99; DB 13; Length 357;
Best Local Similarity 41.1%; Pred. NO. 0.00074;
Matches 23; Conservative 13; Mismatches 18; Indels 2; Gaps 2;

QY 7 ISCFQQIYGVVYGNVTHFVPSNPLKVLWKOKDKVAELE-NSEFRATSSFKNR 61
DB 22 IYC-BEKVFGILGENTFFVKADNKIDVITKDKVAEWAQSEPTYFNSLSR 76

RESULT 9
O9U2P8 PRELIMINARY; PRT; 546 AA.
AC O9U2P8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Y26D4A.10 protein.
GN Y26D4A.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: AL110478; CAB54346.1; -.
DR WormPep: Y26D4A.10; CE21490.
SQ SEQUENCE 546 AA; 63551 MW; 191A4A7B76B06261 CRC64;

Query Match 20.5%; Score 67; DB 5; Length 546;
Best Local Similarity 28.4%; Pred. NO. 9.9;
Matches 21; Conservative 11; Mismatches 26; Indels 16; Gaps 3;

QY 2 HCGFTSCFSQQIYGVVY-----GNVTHFVPSNPLKVLWKQ--KDKV--A 45
DB 165 HIFGFEVCYKIIYGRKHNLSYRSPENKNSITSSNPQNTAKMVINKLQWIPKIPCL 224

QY 46 ELENSFRAFSSFK 59
DB 225 EMONKLINIFESNK 238

RESULT 10
O8GN34 PRELIMINARY; PRT; 108 AA.
AC O8GN34;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tetracycline resistance protein Tet37.
GN Tet37.
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
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[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:47:23 ; Search time 6.1299 Seconds
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421.045 Million cell updates/sec

Title: US-09-730-465-2_COPY_20_80

Perfect score: 327

Sequence: 1 LHCFFGFCFSQIYGVVIG.....DKVAELENSEFRAFSSFKNR 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA: *
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	240	1	US-07-940-861-12
2	327	100.0	240	1	US-08-459-512-12
3	327	100.0	240	2	US-08-459-657-12
4	327	100.0	240	2	US-08-460-132-12
5	327	100.0	240	3	US-08-466-465-4
6	327	100.0	240	5	PCT-US92-02050-12
7	327	100.0	240	6	5185441-36
8	327	100.0	240	6	5223394-4
9	327	100.0	240	6	5223394-6
10	327	100.0	250	1	US-07-940-861-10
11	327	100.0	250	1	US-08-459-512-10
12	327	100.0	250	2	US-08-459-657-10
13	327	100.0	250	2	US-08-460-132-10
14	327	100.0	250	3	US-08-466-465-2
15	327	100.0	250	5	PCT-US92-02050-10
16	327	100.0	250	6	5223394-1
17	327	100.0	251	6	5185441-38
18	327	100.0	347	1	US-07-940-861-43
19	327	100.0	347	1	US-08-459-512-43
20	327	100.0	347	2	US-08-459-657-43
21	327	100.0	347	2	US-08-460-132-43
22	327	100.0	347	3	US-08-466-465-8
23	327	100.0	347	5	PCT-US92-02050-43
24	316	96.6	77	1	US-07-940-861-5
25	316	96.6	77	1	US-08-459-512-5
26	316	96.6	77	2	US-08-459-657-5
27	316	96.6	77	2	US-08-460-132-5

28 316 96.6 77 5 PCT-US92-02050-5
29 271 82.9 134 1 US-08-328-152A-13
30 271 82.9 222 1 US-08-328-152A-6
31 260 79.5 50 1 US-07-940-861-2
32 260 79.5 50 1 US-08-459-512-2
33 260 79.5 50 2 US-08-459-657-2
34 260 79.5 50 2 US-08-460-132-2
35 260 79.5 50 5 PCT-US92-02050-2
36 200 61.2 38 6 5185441-1
37 143.5 43.9 131 1 US-08-328-152A-1
38 143.5 43.9 199 1 US-08-328-152A-36
39 143.5 43.9 225 1 US-08-328-152A-31
40 62 19.0 29 1 US-08-328-152A-3
41 60.5 18.5 373 4 US-09-724-864-43
42 59.5 18.2 288 4 US-09-651-200-14
43 57.5 17.6 272 4 US-09-325-932A-156
44 56.5 17.3 179 4 US-09-513-057C-24
45 56.5 17.3 317 4 US-08-913-159-14

ALIGNMENTS

RESULT 1
US-07-940-861-12
; Sequence 12, Application US/07940861
; Patent No. 5547853
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,861
; FILING DATE: 21-OCT-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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Sequence 13, Appl1
Sequence 8, Appl1
Sequence 2, Appl1
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Patent No. 5185441
Sequence 1, Appl1
Sequence 36, Appl1
Sequence 31, Appl1
Sequence 3, Appl1
Sequence 43, Appl1
Sequence 14, Appl1
Sequence 156, Appl1
Sequence 24, Appl1
Sequence 14, Appl1

MOLECULE TYPE: protein

US-07-940-861-12

Query Match 100.0%; Score 327; DB 1; Length 240;

Best Local Similarity 100.0%; Pred. No. 1.1e-34;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHCFGFISCFSSQIYGVVGNVTFHVPSPVPLKEVLWKKQDKVAELENSEFRASFKN 60

Db 20 LHCFGFISCFSSQIYGVVGNVTFHVPSPVPLKEVLWKKQDKVAELENSEFRASFKN 79

QY 61 R 61

Db 80 R 80

RESULT 2

US-08-459-512-12

; Sequence 12, Application US/08459512

; Patent No. 5728677

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; APPLICANT: WALLNER, Barbara P.

; APPLICANT: MILLER, Glenn T.

; APPLICANT: ROSA, Margaret D.

; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 875 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022-6250

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,512

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02050

; FILING DATE: 12-MAR-1992

; APPLICATION NUMBER: US 07/667,971

; FILING DATE: 12-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/770,967

; FILING DATE: 07-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: HALEY, James F., Jr.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: B151CIP2

; TELEPHONE: (212)715-0600

; TELEFAX: (212)715-0673

; TELEX: 14-8367

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 240 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-459-512-12

Query Match

Best Local Similarity 100.0%; Score 327; DB 1; Length 240;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 LHCFGFISCFSSQIYGVVGNVTFHVPSPVPLKEVLWKKQDKVAELENSEFRASFKN 79

QY 61 R 61

Db 80 R 80

RESULT 3

US-08-459-657-12

; Sequence 12, Application US/08459657

; Patent No. 5914111

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; APPLICANT: WALLNER, Barbara P.

; APPLICANT: MILLER, Glenn T.

; APPLICANT: ROSA, Margaret D.

; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Neave

; STREET: 875 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022-6250

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,657

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/02050

; FILING DATE: 12-MAR-1992

; APPLICATION NUMBER: US 07/667,971

; FILING DATE: 12-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/770,967

; FILING DATE: 07-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: HALEY, James F., Jr.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: B151CIP2

; TELEPHONE: (212)715-0600

; TELEFAX: (212)715-0673

; TELEX: 14-8367

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 240 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-459-657-12

Query Match

Best Local Similarity 100.0%; Score 327; DB 2; Length 240;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 LHCFGFISCFSSQIYGVVGNVTFHVPSPVPLKEVLWKKQDKVAELENSEFRASFKN 79

QY 61 R 61

Db 80 R 80

RESULT 2
 US-09-730-465-4
 ; Sequence 4, Application US/09730465
 ; Patent No. US20020009449A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wallner, Barbara P.
 ; ; Cooper, Kevin D.
 ; TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
 ; Presenting Cell Driven Skin Conditions Using
 ; Inhibitors of the CD2/LFA-3 Interaction
 ;
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/730,465
 ; FILING DATE: 05-Dec-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/08755
 ; FILING DATE: 06-OCT-1992
 ; APPLICATION NUMBER: US 07/862,022
 ; FILING DATE: 12-APR-1992
 ; APPLICATION NUMBER: US 07/770,969
 ; FILING DATE: 07-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Myers, Louis (PLM)
 ; REGISTRATION NUMBER: 35,965
 ; REFERENCE/DOCKET NUMBER: BGP-111CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-5941
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 240 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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 ; US-09-730-465-4
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 ; Query Match 100.0%; Score 327; DB 9; Length 240;
 ; Best Local Similarity 100.0%; Pred. No. 3.8e-34;
 ; Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ; |
 ; Db 20 LHCFCGFCISQSIYGVYGNVTFHVPNSVPLKEVLWKQDKVAELENSEFRAFSFKN 79
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 ; QY 61 R 61
 ; |
 ; Db 80 R 80
 ;
 ; RESULT 3
 ; US-09-796-033-2
 ; Sequence 2, Application US/09796033
 ; Patent No. US20020009446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Macilavy, Daniel
 ; TITLE OF INVENTION: METHOD OF MODULATING MEMORY EFFECTOR
 ; TITLE OF INVENTION: T-CELLS AND COMPOSITIONS
 ; FILE REFERENCE: 10274-044001
 ; CURRENT APPLICATION NUMBER: US/09/796,033

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 11:24:22 ; Search time 81 Seconds
(without alignments)
31.353 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 360314

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	42.9	16	23	AAE23846 Human zsig33-gamma
2	36	42.9	16	23	AAE23847 Human zsig33-gamma
3	36	42.9	16	23	AAE15891 Human zsig33-gamma
4	36	42.9	16	23	AAE15892 Human zsig33-gamma
5	35	41.7	15	16	AAE15893 Human zsig33-gamma
6	35	41.7	15	23	AAE15894 Human zsig33-gamma
7	34	40.5	10	21	AAE15895 Human zsig33-gamma
8	34	40.5	15	23	AAE15896 Human zsig33-gamma
9	34	40.5	15	23	AAE15897 Human zsig33-gamma

10	34	40.5	15	24	ABR33624 Human cancer-relat
11	34	40.5	15	24	ABR33657 Human cancer-relat
12	34	40.5	15	24	ABR33676 Human cancer-relat
13	34	40.5	15	24	ABR33694 Human cancer-relat
14	34	40.5	15	24	ABR33717 Human cancer-relat
15	34	40.5	15	24	ABR33753 Human cancer-relat
16	34	40.5	15	24	ABR33764 Human cancer-relat
17	32	38.1	14	22	AAU76027 Human peptide #179
18	32	38.1	16	15	AAU76027 Pair 3, Pep 5 immun
19	31	36.9	8	23	AAU76075 Nociceptin-like im
20	31	36.9	9	23	AAU76074 Nociceptin-like im
21	31	36.9	10	22	AAU76073 Amino acid sequenc
22	31	36.9	10	23	ABP53304 Gene delivery rela
23	31	36.9	11	23	AAU76110 Nociceptin-like pe
24	31	36.9	12	23	AAU76099 Nociceptin-like pe
25	31	36.9	12	23	AAU76102 Nociceptin-like pe
26	31	36.9	12	23	AAU76106 Nociceptin-like pe
27	31	36.9	12	23	AAU76107 Nociceptin-like pe
28	31	36.9	12	23	AAU76112 Nociceptin-like pe
29	31	36.9	13	23	AAU76111 Nociceptin-like pe
30	31	36.9	14	18	AAU76111 Nucleic acid (NA)
31	31	36.9	14	22	AAU76111 Human peptide #195
32	31	36.9	14	22	AAU76111 Human protein frag
33	31	36.9	15	23	ABP53305 Gene delivery rela
34	31	36.9	16	21	AAU76264 yes-encoded oncopr
35	30	35.7	8	18	AAU76264 Anti-fungal peptid
36	30	35.7	8	20	AAU76264 Anti-fungal peptid
37	30	35.7	8	22	AAU76264 Anti-fungal peptid
38	30	35.7	9	17	AAU76264 Anti-fungal peptid
39	30	35.7	9	18	AAU76264 Anti-fungal peptid
40	30	35.7	9	20	AAU76264 Anti-fungal peptid
41	30	35.7	9	22	AAU76264 Anti-fungal peptid
42	30	35.7	14	14	AAU76264 Protein S - CMap b
43	30	35.7	16	15	AAU76264 CytA-2 beta fragme
44	30	35.7	16	20	AAU76264 Synthetic cytotoxi
45	29	34.5	13	22	AAU76264 Human gene 7 encod

ALIGNMENTS

RESULT 1
AAE23846
ID AAE23846 standard; peptide; 16 AA.
AC AAE23846;
XX AAE23846;
XX AAE23846;
DT 10-SEP-2002 (first entry)
XX Human zsig33-gamma peptide #2.
DE Human zsig33-gamma peptide #2.
XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX Homo sapiens.
XX US200205156-A1.
PN US200205156-A1.
XX US200205156-A1.
XX US200205156-A1.
PD 09-MAY-2002.
XX 09-MAY-2002.
XX 09-MAY-2002.
PF 10-MAY-2001; 2001US-0853253.
XX 10-MAY-2001; 2001US-0853253.
PR 11-MAY-2000; 2000US-203300P.
XX 11-MAY-2000; 2000US-203300P.
XX (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI WPI; 2002-443750/47.

XX	ZSIG33-Like peptides and polynucleotides, useful for modulating gastric contractility, nutrient uptake, growth hormones and/or secretion of digestive/pancreatic enzymes and hormones -
PP	Claim 5; Page 30; 34pp; English.
XX	The invention relates to zsig33-like peptides and their corresponding nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones.
CC	The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression.
CC	The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The ZSIG33 peptides are used as antigens in the production of antibodies against ZSIG33 and in assays to identify modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies and antagonists are used to down regulate expression and activity. The anti-ZSIG33 antibodies are also used as diagnostic agents for detecting the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33-like peptide, zsig33-gamma peptide.
CC	Sequence 16 AA;
SQ	Query Match 42.9%; Score 36; DB 23; Length 16; Best Local Similarity 33.3%; Pred. No. 91; Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY	2 LKEVILKKQDKYAE 16 ::: ::: : : 2 LODILWEEAKEPAD 16
DB	
XX	RESULT 2
AAE23847	ID AAE23847 standard; peptide; 16 AA.
XX	AAE23847;
AC	
XX	10-SEP-2002 (first entry)
DT	
DT	Human zsig33-gamma peptide #3.
DE	
DE	Human; zsig33-like peptide; gastric contractility; nutrient uptake; growth hormone; digestive enzyme; restorative therapy; gene therapy; protein therapy; gastrointestinal; endocrine; anabolic.
KW	Homo sapiens.
KW	OS
XX	US200205156-A1.
PN	XX
PD	09-MAY-2002.
XX	
XX	10-MAY-2001; 2001US-0853253.
XX	
PR	11-MAY-2000; 2000US-203300P.
PA	(JASP/) JASPERS S R.
PA	(SHEP/) SHEPPARD P O.
PA	(DEIS/) DEISHER T A.
PA	(BISH/) BISHOP P D.
XX	Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI	WPI; 2002-443750/47.
DR	
DR	ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT	

PT	contractility, nutrient uptake, growth hormones and/or secretion of
PT	digestive/pancreatic enzymes and hormones -
XX	
XX	Claim 5; Page 30; 34pp; English.
CC	The invention relates to zsig33-like peptides and their corresponding
CC	nucleic acids and methods for modulating gastric contractility, nutrient
CC	uptake, growth hormones, secretion of digestive enzymes and hormones.
CC	The sequences of the invention are used in the prevention, diagnosis and
CC	treatment of diseases associated with inappropriate ZSIG33 expression.
CC	The nucleic acids of the invention and their complements are used as
CC	DNA probes in diagnostic assays to detect and quantitate the presence
CC	of similar nucleic acids in samples, and therefore which patients may be
CC	in need of restorative therapy. The ZSIG33 peptides are used as antigens
CC	in the production of antibodies against ZSIG33 and in assays to identify
CC	modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC	and antagonists are used to down regulate expression and activity. The
CC	anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC	the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC	assay (ELISA)). The peptides and nucleic acids of the invention are used
CC	to modulate gastric contractility, nutrient uptake, growth hormones, the
CC	secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC	and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC	and zsig33-like peptide is used in protein therapy. The present sequence
CC	is human zsig33-like peptide, zsig33-gamma peptide.
XX	
SQ	Sequence 16 AA;
	Query Match 42.9%; Score 36; DB 23; Length 16;
	Best Local Similarity 33.3%; Pred.No. 91;
	Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY	2 LKEVLWKOKDKVAE 16
	: : : : : l : :
DB	2 LQDILWEEAKEPAD 16
	:
RESULT 3	
ID	AAEI5891
ID	AAEI5891 standard; peptide; 16 AA.
AC	AAEI5891;
XX	
XX	26-MAR-2002 (first entry)
XX	
XX	Human zsig33-gamma peptide #2.
DE	
KW	Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
KW	infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
KW	adsorption enhancer; gastrointestinal disease; growth related disease;
KW	inflammation; gene therapy; growth regulation; blood vessel formation;
KW	HIV; zsig33-gamma peptide.
OS	
OS	Homo sapiens.
PN	
PN	WO200187933-A2.
XX	
PD	22-NOV-2001.
PF	
PF	10-MAY-2001; 2001WO-US15091.
XX	
XX	11-MAY-2000; 2000US-0569271.
PR	
XX	(Zymo) ZYMOGENETICS INC.
FA	
XX	Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI	
XX	WPI: 2002-082982/11.
DR	N-PSDB; AAD25764.
DR	
XX	New polypeptides, useful for modulating gastric contractility, nutrient
PT	uptake, pancreatic secretion of hormones, digestive enzymes and
PT	treating gastrointestinal and growth related diseases, comprises
PT	

PT ZSIG33-Like peptides and polynucleotides, useful for modulating gastric

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OM protein - protein search, using sw model

Run on: October 7, 2003, 11:25:08 ; Search time 22 Seconds
(without alignments)
34.201 Million cell updates/sec

Title: US-09-730-465-2_COPY_50_65
Perfect score: 84
Sequence: 1 PLKEVLWKKQDKVAE 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 872

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	23	27.4	15	1	MALT_BACTQ
2	21	25.0	13	1	NO40_PEA
3	21	25.0	13	1	NO40_VICSA
4	21	25.0	13	1	RPOC_MVCGA
5	21	25.0	14	1	MAST_PARID
6	21	25.0	14	1	MAST_POLJA
7	20	23.8	12	1	UR2B_CATCO
8	20	23.8	12	1	UR2B_CTPCA
9	20	23.8	12	1	UR2_POLSP
10	20	23.8	14	1	SMS1_MYOSC
11	20	23.8	14	1	SMS_ALIMI
12	18.5	22.0	14	1	MAST_VESBA
13	18	21.4	10	1	SPI_HALRO
14	18	21.4	11	1	LPW_THETH
15	18	21.4	12	1	NO40_SESRO
16	18	21.4	15	1	PKRH_PHIPA
17	18	21.4	16	1	FIBA_MELME
18	18	21.4	16	1	FIBA_MUSVI
19	17	20.2	7	1	WMA2_ACHFU
20	17	20.2	7	1	WMA3_ACHFU
21	17	20.2	9	1	LPCA_STAAR
22	17	20.2	11	1	CEP1_ACHFU
23	17	20.2	11	1	Q2OA_COMTE
24	17	20.2	12	1	NO40_LOTJA
25	17	20.2	12	1	RS19_CLYEP
26	17	20.2	12	1	RS19_TOBBP
27	17	20.2	12	1	UR2A_CATCO
28	17	20.2	12	1	UR2A_GILMI
29	17	20.2	12	1	UR2_SVCVA
30	17	20.2	13	1	AU11_LITRA
31	17	20.2	13	1	AU12_LITRA
32	17	20.2	14	1	RS19_PRAAP
33	17	20.2	15	1	C10A_RAT

34 17 20.2 15 1 CYSK_CLOPA P81340 clostridium
35 17 20.2 15 1 THL_CLOPA P81347 clostridium
36 17 20.2 15 1 UC27_MAIZE P80633 zea mays (m
37 17 20.2 16 1 MXPX_SOLTU P80501 solanum tub
38 16 19.0 9 1 COW_CONVE P83047 conus ventr
39 16 19.0 9 1 NEF_HVIZ8 P12481 human immun
40 16 19.0 9 1 ULAD_HUMAN P31929 homo sapien
41 16 19.0 10 1 APE_CAFGI P80474 capocytoph
42 16 19.0 10 1 GONL_PETMA P04378 petromyzon
43 16 19.0 10 1 GON3_PETMA P30948 petromyzon
44 16 19.0 12 1 CALM_TETTH Q08055 tetrahymena
45 16 19.0 12 1 NO40_SOYBN P55960 glycine max

ALIGNMENTS

RESULT 1
MALT_BACTQ STANDARD; PRT; 15 AA.
ID MALT_BACTQ STANDARD; PRT; 15 AA.
AC P80072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Maltase (EC 3.2.1.20) (Alpha-glucosidase I) (Fragment).
OS Bacillus thermoamyloliquefaciens.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1425;
RN [1]
RP SEQUENCE.
RC STRAIN=KP1071 / FERM P8477;
RX MEDLINE=92209510; PubMed=1555585;
RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;
RT "Assignment of bacillus thermoamyloliquefaciens KP1071
alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
and in structural parameters calculated from the amino acid
composition.";
RL Eur. J. Biochem. 205:249-256(1992).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
DR PIR: S21240; S21240.
KW Hydrolase; Glycosidase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;
Query Match 27.4%; Score 23; DB 1; Length 15;
Best Local Similarity 37.5%; Pred. No. 8.1e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 LKEVLWKK 9
Db 1 MKRAWKE 8
RESULT 2
NO40_PEA STANDARD; PRT; 13 AA.
ID NO40_PEA STANDARD; PRT; 13 AA.
AC P55959;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40.
GN ENOD40.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=cv. Sparkle; TISSUE=Root nodules;
RX MEDLINE=95036021; PubMed=7948896;
RA Matvienko M., van de Sande K., Yang W.-C., van Kammen A., Bisseling T.,
FR Fransen H.J.;
RT "Comparison of soybean and pea ENOD40 cDNA clones representing genes
RT expressed during both early and late stages of nodule development.";
RL Plant Mol. Biol. 26:487-493(1994).
CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
CC SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
CC DEVELOPMENT.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X81064; -; NOT_ANNOTATED_CDS.
DR Modulation.
KW SEQUENCE 13 AA; 1565 MW; 3C695B6BD8A26C3 CRC64;
SQ
Query Match 25.0%; Score 21; DB 1; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 LKEVLWKK 9
: : :
Db 1 MKFLCWQK 8
RESULT 3
NO40_VICSA STANDARD; PRT; 13 AA.
ID NO40_VICSA
AC P55961;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Early nodulin 40.
EN ENOD40.
GN Vicia sativa (Spring vetch) (Tare).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3908;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nigra; TISSUE=Root nodules;
RX MEDLINE=96011756; PubMed=7548828;
RA Vijn I., Yang W.-C., Pallsigaard N., Oestergaard Jensen E.,
FR van Kammen A., Bisseling T.;
RT "VSEND5, VSEND12 and VSEND40 expression during Rhizobium-induced
RT nodule formation on Vicia sativa roots.";
RL Plant Mol. Biol. 28:1111-1119(1995).
CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
CC SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING RHIZOBIUM-INDUCED NODULE
CC FORMATION. IN 4-DAY OLD NODULES IT IS FOUND IN ALL THE CELLS OF
CC THE CENTRE OF THE NODULE PRIMORDIUM AND ALSO OCCURS IN THE REGION
CC OF THE ROOT PERICYCLE FACING THE NODULE PRIMORDIUM. AT DAY 5,
CC EXPRESSION IS SEEN IN THE COMPLETE CENTRAL TISSUE. AT DAY 20
CC EXPRESSED IN THE COMPLETE PREFIXATION ZONE II, AND IN THE PROXIMAL
CC PART OF THIS ZONE IT IS FOUND ONLY IN THE INFECTED CELLS BUT NOT
CC IN THE UNINFECTED CELLS. AT THE TRANSITION OF PREFIXATION ZONE II
CC INTO INTERZONE II-III EXPRESSION DECREASES IN THE INFECTED CELLS.
CC IN THE FIXATION ZONE III, EXPRESSION IS INDUCED IN THE UNINFECTED
CC CELLS AND IN THE PROXIMAL PART OF THIS ZONE IT IS UNDETECTABLE.
CC PRESENT AT HIGH LEVELS IN THE PERICYCLE OF THE NODULE VASCULAR
CC BUNDLE.

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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X83683; CAB37926.1; -;
DR PIR: S60046; S60046.
KW Modulation.
SQ SEQUENCE 13 AA; 1531 MW; 3C6953C4BD8A26C3 CRC64;
Query Match 25.0%; Score 21; DB 1; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 LKEVLWKK 9
: : :
Db 1 MKFLCWQK 8
RESULT 4
RPOC_MYCGA STANDARD; PRT; 13 AA.
ID RPOC_MYCGA
AC P47716;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit) (Fragment).
GN RPOC.
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AS969Var.B;
RA Skamrov A.V., Feoktistova E.S., Gol'dman M.A., Feoktistova E.S.,
RA Bibilashvili R.S.;
RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
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CC
CC EMBL; L38402; AAB40952.1; -;
DR Transferrase; DNA-directed RNA polymerase; Transcription.
FT NONTER 13 13
SQ SEQUENCE 13 AA; 1630 MW; 4BEC27C7480DA333 CRC64;
Query Match 25.0%; Score 21; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 KKKQDK 13
: : :
Db 6 KKKNK 11

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OM protein - protein search, using sw model

Run on: October 7, 2003, 11:25:43 ; Search time 92 Seconds
(without alignments)
44.879 Million cell updates/sec

Title: US-09-730-465-2_COPY_50_65

Perfect score: 84
Sequence: 1 PLKEVLKKQDKVAE 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 4022

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	34.5	15	5 P82207	P82207 bombyx mori
2	27	32.1	14	2 Q47599	Q47599 escherichia
3	26	31.0	15	4 Q9UC07	Q9UC07 homo sapien
4	25	29.8	15	3 Q9URE0	Q9URE0 saccharomyc
5	24.5	29.2	13	2 Q9R8R9	Q9R8R9 streptococc
6	23	27.4	12	11 Q8CJ30	Q8CJ30 mus musculu
7	23	27.4	15	2 Q9R5L9	Q9R5L9 bacillus st
8	23	27.4	15	10 Q9SRV2	Q9SRV2 triticum ae
9	22	26.2	12	5 Q61574	Q61574 osteragia
10	21	25.0	12	10 Q93WF2	Q93WF2 lupinus lut
11	21	25.0	15	2 Q9R586	Q9R586 serratia ma
12	21	25.0	15	2 Q05991	Q05991 staphylococ
13	21	25.0	15	6 Q9GLJ0	Q9GLJ0 sus scrofa
14	21	25.0	16	4 Q81WX4	Q81WX4 homo sapien
15	21	25.0	16	11 Q9CTB2	Q9CTB2 mus musculu
16	20	23.8	9	4 Q9UNAO	Q9UNAO homo sapien

17	20	23.8	11	2 Q56413	Q56413 escherichia
18	20	23.8	11	4 Q9H4H5	Q9H4H5 homo sapien
19	20	23.8	11	4 Q9UE69	Q9UE69 homo sapien
20	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
21	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
22	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
23	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
24	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
25	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
26	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
27	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
28	20	23.8	12	13 Q8JHCL	Q8JHCL cyprinus ca
29	19	22.6	9	2 Q93E20	Q93E20 streptococc
30	19	22.6	10	13 Q9PRU1	Q9PRU1 cynops pyrr
31	19	22.6	12	2 Q8VLX8	Q8VLX8 thermus the
32	19	22.6	12	10 Q93WB7	Q93WB7 lupinus lut
33	19	22.6	12	10 Q81LCL	Q81LCL trifolium f
34	19	22.6	12	11 Q83579	Q83579 rattus norv
35	19	22.6	12	11 Q83579	Q83579 rattus norv
36	19	22.6	14	2 Q9R3U3	Q9R3U3 cauliflowe
37	19	22.6	15	2 Q9S0V1	Q9S0V1 nitroge fi
38	19	22.6	15	4 Q9UBK0	Q9UBK0 homo sapien
39	19	22.6	15	15 Q8UM88	Q8UM88 human immun
40	19	22.6	16	4 Q9NZH9	Q9NZH9 homo sapien
41	19	22.6	16	4 Q9UD41	Q9UD41 homo sapien
42	19	22.6	16	11 Q9QW74	Q9QW74 mus sp. hom
43	18	21.4	9	2 P82568	P82568 streptococc
44	18	21.4	10	2 Q8RIT1	Q8RIT1 anaplasma p
45	18	21.4	10	4 Q8WTT4	Q8WTT4 homo sapien

ALIGNMENTS

RESULT 1
ID P82207 PRELIMINARY; PRT; 15 AA.
AC P82207;
DT 01-OCT-2001 (TREMREL. 18, Created)
DT 01-OCT-2001 (TREMREL. 18, Last sequence update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "protein database for several tissues derived from five instar of
RT silkworm.";
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1877 MW; 580F6BD4703CA70C CRC64;
Query Match 34.5%; Score 29; DB 5; Length 15;
Best Local Similarity 35.7%; Pred. No. 6.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 3 KEVLKKQDKVAE 16
DB 2 KSLFTQKQYDINE 15
RESULT 2
ID Q47599 PRELIMINARY; PRT; 14 AA.
AC Q47599;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)

01-NOV-1998 (TReMBLrel. 08, Last annotation update)
C (Fragment).
Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
[1]
RN
SEQUENCE FROM N.A.
MEDLINE=91139577; PubMed=1995588;
Tao T., Bourne J.C., Blumenthal R.M.;
"A family of regulatory genes associated with type II restriction-
modification systems.";
J. Bacteriol. 173:1367-1375(1991).
J. Bacteriol. 173:1367-1375(1991).
EMBL: M63619; AAA24555.1; -
NON_TER 1
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SEQUENCE 14 AA; 1705 MW; 77B6CA60581A4F3B CRC64;
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Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
2Y 2 LKEVLWKQKD 12
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Db 1 LKEVINERKKHE 11
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ID Q9UCC7
AC Q9UCC7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Midkine (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN
SEQUENCE
MEDLINE=94059921; PubMed=82411100;
Novotny W.F., Marfi T., Mehta R.L., Milner P.G.;
"Identification of novel heparin-releasable proteins, as well as the
cytokines midkine and pleiotrophin, in human postheparin plasma.";
Arterioscler. Thromb. 13:1798-1805(1993).
SEQUENCE 15 AA; 1527 MW; C34B6B97878474AC CRC64;
Query Match 31.0%; Score 26; DB 4; Length 15;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 KOKDXV 14
|:||||
Db 3 KKKDXV 8
|:||||
RESULT 4
Q9URE0 PRELIMINARY; PRT; 15 AA.
ID Q9URE0
AC Q9URE0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Type II topoisomerase, topoisomerase II (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
NCBI_TaxID=4932;
[1]
RN
SEQUENCE FROM N.A.
MEDLINE=95130576; PubMed=7829529;
Elsea S.H., Hsiung Y., Nitiss J.L., Osheroff N.;

J. Biol. Chem. 270:1913-1920(1995).
NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 2094 MW; 0A6A37F6B81B85F6 CRC64;
Query Match 29.8%; Score 25; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
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:|:|:|:|:
Db 2 YQKRKDYMSE 11
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ID Q9R8R9
AC Q9R8R9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE C5a peptidase (Fragment).
GN SCPA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF1;
RX MEDLINE=98298075; PubMed=9632622;
RA Berge A., Rasmussen M., Bjorck L.;
"Identification of an insertion sequence located in a region encoding
virulence factors of Streptococcus pyogenes.";
RL Infect. Immun. 66:3449-3453(1998).
DR EMBL: AF064540; AAC38768.1; -
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FT NON_TER 13
SQ SEQUENCE 13 AA; 1603 MW; 5EDADCD6ACE6723 CRC64;
Query Match 29.2%; Score 24.5; DB 2; Length 13;
Best Local Similarity 63.6%; Pred. No. 3e+03; 1; Mismatches 0; Indels 3; Gaps 1;
Matches 7; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
QY 8 KQKQ--DKVA 15
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Db 3 KQKQLPFDKLA 13
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ID Q8CJ30
AC Q8CJ30;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Myonaurin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RX MEDLINE=20334280; PubMed=10873615;
RA Alliel P.M., Seddigi N., Goudou D., Cifuentes-Diaz C., Romero N.,
RA Velasco E., Rieger F., Perin J.P.;
RT "Myonaurin, a novel member of the BTB/POZ-zinc finger family highly
expressed in human muscle.";
RL Biochem. Biophys. Res. Commun. 273:385-391(2000).
[2]
RN
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Bitoun M., Perin J.P., Seddigi N., Goudou D., Camuzat A., Mattei M.G.;

NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UM-03314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1
OTHER INFORMATION: /note= "The residue at this position is bound to an Alkaloid by a sulfide."
US-09-050-811-5
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Best Local Similarity 71.4%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 WKKQKDK 13
DB 2 WKKKKKK 8
RESULT 3
US-09-050-811-6
Sequence 6, Application US/09050811
Patent No. 6387700
GENERAL INFORMATION:
APPLICANT: Rice, Kevin G.
APPLICANT: Wadhwa, Manpreet S.
TITLE OF INVENTION: Peptides for Gene Delivery
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,811
FILING DATE: 30-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UM-03314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1
OTHER INFORMATION: /note= "The residue at this position is bound to an Alkaloid by a Sulfide."

US-09-050-811-6
Query Match 36.9%; Score 31; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 WKKQKDK 13
DB 2 WKKKKKK 8
RESULT 4
US-09-050-811-11
Sequence 11, Application US/09050811
Patent No. 6387700
GENERAL INFORMATION:
APPLICANT: Rice, Kevin G.
APPLICANT: Wadhwa, Manpreet S.
TITLE OF INVENTION: Peptides for Gene Delivery
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,811
FILING DATE: 30-MAR-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UM-03314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-050-811-11
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Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 2 WKKKKKK 8
RESULT 5
US-08-621-259A-205
Sequence 205, Application US/08621259A
Patent No. 5858974
GENERAL INFORMATION:
APPLICANT: Little II, Roger G
APPLICANT: Lim, Edward
APPLICANT: Padem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
NUMBER OF SEQUENCES: 252
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 11:31:08 ; Search time 67 Seconds
(without alignments)
37.782 Million cell updates/sec

Title: US-09-730-465-2_COPY_50_65
Perfect score: 84
Sequence: 1 PLKEVLWKKQDKVAE16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 107419

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Minimum DB seq length: 0
Maximum DB seq length: 16
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	42.9	16	9	US-09-853-253-15	Sequence 15, Appl
2	36	42.9	16	9	US-09-853-253-16	Sequence 16, Appl
3	34	40.5	15	9	US-09-853-253-17	Sequence 17, Appl
4	31	36.9	8	11	US-09-882-291-63	Sequence 63, Appl
5	31	36.9	9	11	US-09-882-291-61	Sequence 61, Appl
6	31	36.9	10	12	US-10-108-844-5	Sequence 5, Appl
7	31	36.9	11	11	US-09-882-291-55	Sequence 55, Appl
8	31	36.9	12	11	US-09-882-291-35	Sequence 35, Appl
9	31	36.9	12	11	US-09-882-291-50	Sequence 50, Appl
10	31	36.9	12	11	US-09-882-291-53	Sequence 53, Appl
11	31	36.9	13	11	US-09-882-291-56	Sequence 56, Appl
12	31	36.9	15	12	US-10-108-844-6	Sequence 6, Appl
13	31	36.9	15	12	US-10-108-844-11	Sequence 11, Appl
14	30	35.7	9	9	US-09-881-490-163	Sequence 163, Appl
15	29	34.5	15	9	US-09-765-537-101	Sequence 101, Appl

16	29	34.5	15	12	US-10-014-322A-90	Sequence 90, Appli
17	28	34.5	15	11	US-10-106-698-7620	Sequence 38, Appl
18	29	33.5	12	15	US-09-882-291-320	Sequence 38, Appl
19	28	33.3	12	12	US-09-870-498A-1	Sequence 1, Appli
20	28	33.3	13	12	US-10-224-356-32	Sequence 32, Appl
21	28	33.3	14	12	US-10-224-356-34	Sequence 34, Appl
22	28	33.3	14	12	US-10-020-269-23	Sequence 23, Appl
23	28	33.3	15	12	US-10-014-322A-100	Sequence 100, Appl
24	28	33.3	16	15	US-10-225-567A-1191	Sequence 1191, Ap
25	27	32.1	9	12	US-10-356-828-33	Sequence 33, Appl
26	27	32.1	10	11	US-09-572-404B-663	Sequence 663, App
27	27	32.1	10	11	US-09-572-404B-665	Sequence 665, App
28	27	32.1	12	11	US-09-876-904A-247	Sequence 247, App
29	27	32.1	15	15	US-10-264-303-15	Sequence 15, Appl
30	26	31.0	9	10	US-09-071-838-74	Sequence 74, Appl
31	26	31.0	9	15	US-10-213-513-74	Sequence 74, Appl
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36	26	31.0	11	10	US-09-791-378-302	Sequence 302, App
37	26	31.0	11	15	US-10-116-391-10	Sequence 10, Appl
38	26	31.0	12	15	US-10-216-810A-5	Sequence 5, Appli
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40	26	31.0	13	12	US-10-153-244-119	Sequence 119, App
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42	26	31.0	13	12	US-10-153-244-218	Sequence 218, App
43	26	31.0	13	15	US-10-211-088-232	Sequence 232, App
44	26	31.0	14	9	US-09-766-396-8	Sequence 8, Appli
45	26	31.0	14	14	US-10-063-375-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-09-853-253-15
  / Sequence 15, Application US/09853253
  / Patent No. US20020055156A1
  / GENERAL INFORMATION:
  / APPLICANT: JASPER, STEPHEN
  / APPLICANT: SHEPPARD, PAUL
  / APPLICANT: DEISHER, THERESA
  / APPLICANT: BISHOP, PAUL
  / TITLE OF INVENTION: zsig33-like Peptides
  / FILE REFERENCE: 00-30
  / CURRENT APPLICATION NUMBER: US/09/853,253
  / CURRENT FILING DATE: 2001-05-10
  / PRIOR APPLICATION NUMBER: 60/203,300
  / PRIOR FILING DATE: 2000-05-11
  / NUMBER OF SEQ ID NOS: 28
  / SOFTWARE: FastSEQ for Windows Version 3.0
  / SEQ ID NO 15
  / LENGTH: 16
  / TYPE: PrT
  / ORGANISM: Homo sapiens
US-09-853-253-15

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Query Match 42.9%; Score 36; DB 9; Length 16;
Best Local Similarity 33.3%; Pred. No. 56;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Db      2 LODILWEEAKEAPAD 16
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RESULT 2
US-09-853-253-16
; Sequence 16, Application US/09853253
; Patent No. US200205156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN

```
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig333-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (16)...(16)
;
US-09-853-253-16

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Best Local Similarity 33.3%; Pred. No. 56;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKEVLWKQKQKVAE 16
|::|::|: |: |:
Db 2 LQDILWEEAKEAPAD 16

RESULT 3
US-09-853-253-17
; Sequence 17, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; TITLE OF INVENTION: Zsig333-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (15)...(15)
;
US-09-853-253-17

Query Match 40.5%; Score 34; DB 9; Length 15;
Best Local Similarity 35.7%; Pred. No. 1e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKEVLWKQKQKVA 15
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Db 2 LQDILWEEAKEAPA 15

RESULT 4
US-09-882-291-63
; Sequence 63, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequen

US-09-882-291-61
; Sequence 61, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequen

US-09-882-291-61

Query Match 36.9%; Score 31; DB 11; Length 8;
Best Local Similarity 71.4%; Pred. No. 5.2e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 WKQKQDK 13
|::|::|: |
Db 2 WKKKKKK 8

RESULT 5
US-09-882-291-61
; Sequence 61, Application US/09882291
; Publication No. US20030040472A1
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates
; FILE REFERENCE: 007-2001
; CURRENT APPLICATION NUMBER: US/09/882,291
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequen

US-09-882-291-61

Query Match 36.9%; Score 31; DB 11; Length 8;
Best Local Similarity 71.4%; Pred. No. 5.2e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 WKQKQDK 13
|::|::|: |
Db 2 WKKKKKK 8

RESULT 6
US-10-108-844-5
; Sequence 5, Application US/10108844
; Publication No. US20030170894A1
; GENERAL INFORMATION:
; APPLICANT: Rice, Kevin G.
; TITLE OF INVENTION: Peptides for Gene Delivery
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/108,844
; FILING DATE: 28-Mar-2002
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:34:43 ; Search time 102.059 Seconds
(without alignments)
539.670 Million cell updates/

Title: US-09-730-465-8

Perfect score: 1856

Sequence: 1 MVAGSDAGRALGVLSVVCLL.....MHEALHNHYTQKSLSLSPGK 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMÀRIES

Result No.	Query %	Score	Match	Length	DB	ID	Description
1	1856	100.0	347	13	AAK27163		CD2 binding LFA-3-
2	1856	100.0	347	21	AAV83136		Human transmembran
3	1856	100.0	347	22	AA961160		Human LFA3TIP fusi
4	1856	100.0	347	23	ABG71056		Human lymphocyte f
5	1856	100.0	347	23	AB981994		Human LFA3TIP poly
6	1856	100.0	347	23	AB576228		LFA3/1gg fusion pr
7	1856	100.0	347	24	ABF58278		Murine LFA-3. Mus
8	1845	99.4	351	23	AB981995		Human LFA-3/Tgg fu
9	1834	98.8	347	14	AAK34224		Amino acid sequenc

Murine CD2-binding
FtL1 receptor fusi
Modified FtL1 rece
FtL123_Flk1D3_FcD
FtL1 receptor fusi
FtL1 receptor fusi
Modified FtL1 rece
Human ACAM-1/1g
Human amino acid
hB7.2Fc soluble fu
Human TGFbetaRI:F
Amino acid sequen
Rabbit TGFbetaRI:
Amino acid sequen
Human FGF-R1 Extra
Human gp130-Fc-His
Human gp130-Fc-His
Fusion polypeptide
Fusion polypeptide
FtL1 receptor fusi
Modified FtL1 rece
Human Ryk fragment
Concatameric immu
VCAM 2D-1gG. Humo
VCAM 2D-1gG. a sol
VCAM 2D-1gG. a sol
VCAM 2D-1gG protei
A VCAM 2D-1gG fusi
Human VCAM-1/1gG f
B7-related protein
B7-related protein
B7-related protein
B7-related protein
B7-related protein
hB7.1Fc soluble fu
Human expressed p
Integrin alpha2 c

ALIGNMENTS

RESULT 1	
AAR27163	
ID	AAR27163 standard; Protein; 347 AA.
XX	
AC	AAR27163;
XX	
XX	
DT	25-MAR-2003 (updated)
DT	20-MAY-1998 (first entry)
DT	
XX	
XX	
DE	CD2 binding LFA-3-Ig fusion protein.
XX	
XX	
XX	
XX	lymphocyte associated antigen-3; T-lymphocyte
XX	differential mutant; CD2 binding site; immunomod-
XX	preLFA3IP; LFA-3(92)IgG; pSAB152; ss.
XX	
OS	Homo sapiens.
XX	
XX	
PH	Key
FT	Location/Qualifiers
FT	1..28
FT	/label= LFA-3_signal
FT	region
FT	29..120
FT	/label= LFA-3_aminoacids_1-92
FT	region
FT	121..130
FT	/label= IgG1_hinge
FT	131..239
FT	/label= IgG1_CH2
FT	240..347
FT	/label= IgG1_CH3
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XX	
XX	EP503648-A1.
XX	
XX	
PD	16-SEP-1992.

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XX 12-MAR-1992; 92EP-0104320.
XX PF
XX 12-MAR-1991; 91US-0667971.
XX PR
XX 07-OCT-1991; 91US-0770967.
XX PR
XX (BIOJ ) BIOGEN INC.
XX PA
XX Miller GT, Rosa MD, Wallner BP;
XX PI
XX WPI; 1992-309760/38.
XX DR
XX N-PSDB; AAQ28684.
XX DR
XX
XX CD2-binding domain of lymphocyte function associated antigen-3
XX PT
XX and DNA - for diagnosing and treating inflammation and
XX PT
XX auto-immune diseases, e.g. systemic lupus erythematosus and
XX PT
XX rheumatoid arthritis
XX PT
XX
XX Claim 13; Fig 12; 85pp; English.
XX PA
XX
XX The plasmid pSAB152 contains the DNA sequence encoding the LFA-3
XX CC
XX signal sequence, the amino terminal 92 amino acids of mature LFA-3,
XX CC
XX ten amino acids of the hinge region of IgG1 and the CH2 and CH3
XX CC
XX constant domains of IgG1 (See AAQ28678-9 and AAQ28681-2 for details of
XX CC
XX the construction of pSAB152). A NotI fragment containing the coding
XX CC
XX sequence of pSAB152 was used in the construction of expression
XX CC
XX vector pMDR(92)Ig-3 which can be stably maintained in CHO cells to
XX CC
XX achieve continuous expression of LFA3TIP. The fusion protein can
XX CC
XX bind to CD2 and inhibit T cell activation, making it useful to
XX CC
XX treat acute and chronic inflammation, autoimmune disease and
XX CC
XX in immunomodulation.
XX CC
XX (Updated on 25-MAR-2003 to correct PN field.)
XX CC
XX
XX Sequence 347 AA;
XX
XX
XX Query Match 100.0%; Score 1856; DB 13; Length 347;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-128;
XX Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Db
XX 1 MVAGSDAGRALGVLGVVCLLHCFGFCFSQOIYGVVGNVTFHVPSPNPLKEVLWKKQK 60
XX
XX QY 61 DKVAELENSEFRASFSSFKNRVYLDTVSGSLTYNLTSSDEDEYEMESPNITDTMKFFLYV 120
XX Db
XX 61 DKVAELENSEFRASFSSFKNRVYLDTVSGSLTYNLTSSDEDEYEMESPNITDTMKFFLYV 120
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XX QY 121 DKTHTCPPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 180
XX Db
XX 121 DKTHTCPPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 180
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XX Db
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XX
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XX Db
XX 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDLS 300
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XX Db
XX 301 DGSFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 347
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XX RESULT 2
XX AAY83136
XX ID AAY83136 standard; Protein; 347 AA.
XX XX
XX AC AAY83136;
XX XX
XX 24-JUL-2000 (first entry)
XX DT
XX Human transmembrane LFA-3/IgG fusion protein LFA3TIP.
XX DE

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XX LFA3; CD2; cell signalling; modulation; lymphocyte; T cell;
XX KW
XX memory effector T lymphocyte; psoriatic arthritis;
XX KW
XX rheumatoid arthritis; multiple sclerosis; atopic dermatitis;
XX KW
XX uveitis; inflammatory bowel disease; Crohn's disease;
XX KW
XX ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment;
XX KW
XX therapy.
XX
XX OS Homo sapiens.
XX
XX WO200012113-A2.
XX PN
XX
XX 09-MAR-2000.
XX PD
XX
XX 31-AUG-1999; 99WO-US20026.
XX PF
XX
XX 31-AUG-1998; 98US-0098456.
XX PR
XX
XX (BIOJ ) BIOGEN INC.
XX PA
XX
XX Magilavy D;
XX PI
XX
XX WPI; 2000-282928/24.
XX DR
XX N-PSDB; AA293401.
XX
XX Selective modulation of memory effector T lymphocytes by administration
XX PT
XX of a CD2 binding agent which inhibits the CD2/LFA-3 interaction useful
XX PT
XX for treating conditions such as inflammatory bowel diseases, psoriatic
XX PT
XX arthritis
XX
XX Disclosure; Page 75-76; 76pp; English.
XX
XX
XX Modulation of LFA3/CD2 interaction by administration of a CD2 binding
XX CC
XX agent inhibits CD2 signalling and T cell proliferation and activation
XX CC
XX and more particularly modulates the number and/or distribution of
XX CC
XX memory effector T lymphocytes. The method can be used for treating a
XX CC
XX condition in a subject where the condition is characterized by memory
XX CC
XX effector T lymphocytes playing a role in the pathogenesis of the
XX CC
XX condition such as psoriatic arthritis, rheumatoid arthritis,
XX CC
XX multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel
XX CC
XX disease, Crohn's disease, ulcerative colitis and cutaneous T cell
XX CC
XX lymphoma and where the method comprises administering to the subject
XX CC
XX an amount of CD2 binding agent sufficient to modulate the memory
XX CC
XX effector T lymphocytes. The methods provide inhibition of antigen
XX CC
XX specific interactions for all antigens present, inhibition of T cell
XX CC
XX activation, no general immunosuppression, and possibly induction of
XX CC
XX tolerance.
XX
XX Sequence 347 AA;
XX
XX
XX Query Match 100.0%; Score 1856; DB 21; Length 347;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-128;
XX Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 MVAGSDAGRALGVLGVVCLLHCFGFCFSQOIYGVVGNVTFHVPSPNPLKEVLWKKQK 60
XX
XX QY 61 DKVAELENSEFRASFSSFKNRVYLDTVSGSLTYNLTSSDEDEYEMESPNITDTMKFFLYV 120
XX Db
XX 61 DKVAELENSEFRASFSSFKNRVYLDTVSGSLTYNLTSSDEDEYEMESPNITDTMKFFLYV 120
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XX 181 GVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:45:48 ; Search time 42.5245 Seconds
(without alignments)
784.736 Million cell updates/sec

Title: US-09-730-465-8

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Sequence: 1 MVASDAGRALGVLSVYVCLL.....MHEALHNHYTKSLSLSPGK 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	66.4	255	4 S31866	Ig gamma-1 chain C
2	1233	66.4	330	1 GHU	Ig gamma-1 chain C
3	1228.5	66.2	374	2 S89339	Ig heavy chain V r
4	1180	63.6	234	2 P70207	Ig gamma-3 chain C r
5	1146	61.7	377	2 A23511	Ig gamma-2 chain C
6	1145.5	61.7	326	1 G2HU	Ig gamma-3 chain C
7	1144	61.6	377	2 A50764	Ig gamma-3 chain C
8	1135	61.2	327	1 G4HU	Ig gamma-4 chain C
9	1121	60.4	289	1 G3HUI	Ig gamma-3 heavy C
10	926.5	49.9	323	1 GHRB	Ig gamma chain C r
11	913.5	49.2	328	2 I47160	Ig gamma 2b chain
12	909.5	49.0	328	2 I47159	Ig gamma 2a chain
13	906.5	48.8	277	2 I47162	Ig gamma 4 chain c
14	894.5	48.2	328	2 I47158	Ig gamma-2 chain C
15	892	48.1	329	1 G2GP	Ig gamma-2 chain C
16	886.5	47.8	328	2 I47161	Ig gamma 3 chain c
17	857.5	46.2	470	2 S22080	Ig heavy chain pre
18	846	45.6	308	2 C30554	Ig heavy chain C r
19	846	45.6	472	2 S31459	Ig gamma-1 chain -
20	845.5	45.6	329	1 G3MSC	Ig gamma-3 chain C
21	838	45.2	333	2 PS0018	Ig gamma-2b chain
22	834.5	45.0	398	1 G3MSM	Ig gamma-3 chain C
23	829.5	44.7	444	2 P4436	monoclonal antibod
24	819	44.1	326	2 PS0017	Ig gamma-1 chain C
25	818.5	44.1	324	1 G1MS	Ig gamma-1 chain C
26	813.5	43.8	393	1 G1MSM	Ig gamma-1 chain C
27	812	43.8	329	2 S00847	Ig gamma-2c chain
28	811.5	43.7	330	1 G2MSA	Ig gamma-2a chain
29	811.5	43.7	469	2 S37483	Ig gamma-2a chain

Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
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Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2 chain C
Ig gamma heavy cha
lymphocyte functio
Ig heavy chain VHI
Ig heavy chain V-I
Ig gamma-1 chain C
Ig x heavy chain C
Ig epsilon chain C
Ig epsilon chain C

ALIGNMENTS

RESULT 1

S31866
Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C:Accession: S31866

R:Filpula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene pro-

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FIL>

A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

C:Keywords: immunoglobulin

F:1-22/Region: Escherichia coli outer membrane protein A precursor

F:23-255/Region: human Ig gamma-1 chain C region

Query Match 66.4%; Score 1233; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.5e-80;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 DKHTCPCCPAPPELLGGSPSVLEPPPKPKDFLMSRTPEVTCVVVDVSHEDPEVKFNWYD 180

Db 29 DKHTCPCCPAPPELLGGSPSVLEPPPKPKDFLMSRTPEVTCVVVDVSHEDPEVKFNWYD 88

QY 181 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 240

Db 89 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAK 148

QY 241 GQREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 300

Db 149 GQREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 208

QY 301 DGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 347

Db 209 DGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 255

RESULT 2

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982.

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

<p>hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate in C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F; 20-85/Domain: immunoglobulin homology <IM1> F; 137-206/Domain: immunoglobulin homology <IM2> F; 243-310/Domain: immunoglobulin homology <IM3> F; 27-63,144-204,250-308/Disulfide bonds: #status experimental F; 103/Disulfide bonds: interchain (to light chain) #status experimental F; 109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F; 180/Binding site: carbohydrate (Asn) (covalent) #status experimental</p>	
<p>Query Match 66.4%; Score 1233; DB 1; Length 330; Best Local Similarity 100.0%; Pred. No. 2.1e-80; Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	
QY	121 DKTHTCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 180
Db	104 DKTHTCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163
QY	181 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 240
Db	164 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 223
QY	241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTPVLD 300
Db	224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGPENNYKTTTPVLD 283
QY	301 DGSFFLYSKLTVDKSRWQGNVFSCSVAHEALHNHYTKQSLSPGK 347
Db	284 DGSFFLYSKLTVDKSRWQGNVFSCSVAHEALHNHYTKQSLSPGK 330
<p>RESULT 3 S69339 Ig heavy chain V region precursor - human C; Species: Homo sapiens (man) C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000 C; Accession: S69339; S72664 R; Khamlichi, A.A.; Autcourtier, P.; Preud'homme, J.L.; Cogné, M. Eur. J. Biochem. 229, 54-60, 1995 A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition diseases A; Reference number: S69339; MUID:95262687; PMID:774049 A; Accession: S69339 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-374 <KHA> A; Cross-references: EMBL:X81695 R; Khamlichi, A.A. submitted to the EMBL Data Library, September 1994 A; Reference number: S72664 A; Accession: S72664 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-140, 'C', 142-374 <KH2> A; Cross-references: EMBL:X81695 C; Superfamily: immunoglobulin C region; immunoglobulin homology</p>	
<p>Query Match 66.2%; Score 1228.5; DB 2; Length 374; Best Local Similarity 79.3%; Pred. No. 5.2e-80; Matches 234; Conservative 10; Mismatches 22; Indels 29; Gaps 1;</p>	
QY	82 YLDTVSGSLTIYNLTSSDEDEYEMESFNITDITMKFFL----- 118
Db	80 YPSLTRLTRITKDTSRKNQVLTVNTVNDPADTATYICGYSVCGYRFGHSWGGTGLVT 139
QY	119 -----YVDKTHTCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPE 172
Db	140 VSSEPKSCDKTHTCPCPAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPE 199'
QY	173 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPI 232
Db	200 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPI 259

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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:35:28 ; Search time 22.9632 Seconds
(without alignments)
710.626 Million cell updates/sec

Title: US-09-730-465-8

Perfect score: 1856

Sequence: 1 MVAGSDAGRALGVLSVYVCLL.....MHEALHHYTKSLSLSPGK 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1293	66.4	330	1	GCL_HUMAN
2	1145.5	61.7	326	1	GCL_HUMAN
3	1135	61.2	327	1	GCL_HUMAN
4	1126	60.7	290	1	GCL_HUMAN
5	926.5	49.9	323	1	GC_RABIT
6	892	48.1	329	1	GC2_CAVPO
7	845.5	45.6	329	1	GC3_MOUSE
8	838	45.2	333	1	GC3_MOUSE
9	834.5	45.0	398	1	GC3_MOUSE
10	819	44.1	326	1	GCL_RAT
11	818.5	44.1	324	1	GCL_MOUSE
12	813.5	43.8	393	1	GC1_MOUSE
13	812	43.8	329	1	GC3_MOUSE
14	811.5	43.7	330	1	GC3_MOUSE
15	806.5	43.5	399	1	GC3_MOUSE
16	804	43.3	335	1	GC3_MOUSE
17	787.5	42.4	322	1	GC3_MOUSE
18	783.5	42.2	336	1	GC3_MOUSE
19	778.5	41.9	405	1	GC3_MOUSE
20	630	33.9	420	1	LFA3_HUMAN
21	368	19.8	421	1	EPC_MOUSE
22	366.5	19.7	429	1	EPC_MOUSE
23	360.5	19.4	428	1	EPC_MOUSE
24	358.5	19.3	454	1	MUC_MOUSE
25	357	19.2	455	1	MUC_MOUSE
26	356.5	19.2	391	1	MUC_MOUSE
27	351	18.9	458	1	MUC_MOUSE
28	347	18.7	476	1	MUC_MOUSE
29	341	18.4	479	1	MUC_MOUSE
30	335	18.0	457	1	MUC_MOUSE
31	332	17.9	450	1	MUC_MOUSE
32	332	17.9	454	1	MUC_MOUSE
33	302.5	16.3	438	1	HVC2_HETER

34	298.5	16.1	438	1	HVC3_HETER	P23087 heterodontu
35	295.5	15.9	299	1	ALC_RABIT	P01879 oryctolagus
36	291	15.7	446	1	MUC_CHICK	P01875 gallus gall
37	289.5	15.6	461	1	HVC3_HETER	P23088 heterodontu
38	282.5	15.2	393	1	HVC3_HETER	P23086 heterodontu
39	277.5	15.0	370	1	HVC1_HETER	P23084 heterodontu
40	272	14.7	353	1	ALC1_HUMAN	P01876 homo sapien
41	271.5	14.6	340	1	ALC2_HUMAN	P01877 homo sapien
42	268	14.4	353	1	ALC1_GORGO	P20758 gorilla gor
43	257.5	13.9	481	1	MUCM_ICTPU	P23735 ictalurus p
44	245	13.2	344	1	ALC_MOUSE	P01878 mus musculu
45	205	11.0	513	1	SHSL_MOUSE	P97797 m protein-t

ALIGNMENTS

RESULT 1	GCL_HUMAN	STANDARD;	PRT;	330 AA.
ID	GCL_HUMAN			
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DE	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=62274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RN	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RN	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

Intrachain disulfide bonds.";
 Biochemistry 9:3188-3196(1970).
 [7]
 DISULFIDE BONDS.
 RA MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 "Rule of antibody structure. The primary structure of a monoclonal
 IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 characterization of the protein, the L- and H-chains, the
 cyanogen bromide cleavage products, and the disulfide bridges.";
 Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 [8]
 X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RP MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 "Crystallographic refinement and atomic models of a human Fc fragment
 and its complex with fragment B of protein A from *Staphylococcus*
 aureus at 2.9- and 2.8-A resolution.";
 Biochemistry 20:2361-2370(1981).
 RL GLM(1) MARKERS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
 CC MARKER & THE GLM (NON-1) MARKERS.
 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
 CC
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 CC EMBL; J00228; AAC82527.1; ALT_INIT.
 DR PIR; A93433; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR PDB; 1A77; 12-NOV-97.
 DR PDB; 1D5E; 09-FEB-00.
 DR PDB; 1D5I; 09-FEB-00.
 DR PDB; 1D6V; 04-OCT-00.
 DR PDB; 1DN2; 17-MAY-00.
 DR PDB; 1E4K; 06-JUN-01.
 DR PDB; 1FCG; 20-JUL-95.
 DR PDB; 1H2H; 12-JUN-02.
 DR PDB; 1I7Z; 08-AUG-01.
 DR PDB; 1IIS; 16-MAY-01.
 DR PDB; 1IIX; 16-MAY-01.
 DR PDB; 1L6X; 10-APR-02.
 DR PDB; 2RGS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00835; IG-LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 3D-structure.
 KW NON_TER 1 1
 KW DOMAIN 1 98 CH1.
 KW DOMAIN 99 110 HINGE.
 KW DOMAIN 111 223 CH2.

CH3.
 INTERCHAIN (WITH LIGHT CHAIN).
 INTERCHAIN (WITH HEAVY CHAIN).
 INTERCHAIN (WITH HEAVY CHAIN).
 N-LINKED (GLCNAC...).
 REMOVED POST-TRANSLATIONALLY.
 K -> R (IN GLM(3) MARKER).
 /FTIG-VAR_003886.
 D -> E (IN GLM(NON-1) MARKER).
 /FTIG-VAR_003887.
 L -> M (IN GLM(NON-1) MARKER).
 /FTIG-VAR_003888.
 224 330
 27 83
 103 103
 109 109
 112 112
 144 204
 250 308
 180 180
 330 330
 97 97
 239 239
 241 241
 122 126
 130 134
 136 137
 141 147
 157 162
 163 164
 185 166
 188 171
 176 179
 180 181
 182 190
 193 197
 198 199
 202 207
 209 210
 215 219
 227 227
 230 234
 238 242
 245 256
 260 265
 270 270
 274 276
 280 281
 283 284
 287 296
 297 301
 302 303
 305 312
 313 314
 316 317
 320 325
 330 AA; 36106 MW; 3770EEL06C2FA33D CRC64;
 Query Match 66.4%; Score 1233; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.9e-85;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 121 DKTHCTPCPCAPPELLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 180
 DB 104 DKTHCTPCPCAPPELLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 163
 QY 181 GVEVHNATKPREQYNSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPTEKTSKAK 240
 DB 164 GVEVHNATKPREQYNSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPTEKTSKAK 223
 QY 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 300
 DB 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 283
 QY 301 DGSFFLYSKLTVDKSRWQOGNPFSCVMHEALHNHYTQKSLSLSPGK 347
 DB 284 DGSFFLYSKLTVDKSRWQOGNPFSCVMHEALHNHYTQKSLSLSPGK 330
 RESULT 2
 GC2_HUMAN
 ID GC2_HUMAN STANDARD; PRT; 326 AA.

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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:45:18 ; Search time 102.909 Seconds
(without alignments)
870.128 Million cell updates/sec

Title: US-09-730-465-8

Perfect score: 1856
Sequence: 1 MVAGSDAGALGVLSVVCILL.....MHEALHNYTKSLSPGK 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mbc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1233	66.4	471	4	Q8TC77	Q8tc77 homo sapien
2	1233	66.4	701	4	Q96P08	Q96pq8 homo sapien
3	1142	61.5	521	4	Q8N4Y9	Q8n4y9 homo sapien
4	1135	61.2	473	4	Q8TC63	Q8tc63 homo sapien
5	1131	60.9	509	4	Q8NF17	Q8nf17 homo sapien
6	909	49.0	337	6	Q95M34	Q95m34 equus caball
7	831.5	44.8	469	11	Q8R3V9	Q8r3v9 mus musculus
8	830.5	44.7	463	11	Q991C4	Q991c4 mus musculus
9	826.5	44.5	437	11	Q9R1A4	Q9r1a4 mus musculus
10	811	43.7	473	11	Q9D8I4	Q9d8i4 mus musculus
11	807.5	43.5	468	11	Q991J1	Q991j1 mus musculus
12	807.5	43.5	473	11	Q991L25	Q991l25 mus musculus
13	784.5	42.3	473	11	Q91Z05	Q91z05 mus musculus
14	784.5	42.3	474	11	Q8R3H6	Q8r3h6 mus musculus
15	632.5	34.1	240	4	Q9BRW0	Q9brw0 homo sapien
16	476	25.6	134	4	Q14748	Q14748 homo sapien

17	436	23.5	119	4	Q16393	Q16393 homo sapien
18	358.5	19.3	375	4	Q9BSZ1	Q9bsz1 homo sapien
19	358.5	19.3	597	4	Q9BU10	Q9bu10 homo sapien
20	358.5	19.3	597	4	Q9BQB8	Q9bqb8 homo sapien
21	358.5	19.3	597	4	Q96BB9	Q96bb9 homo sapien
22	348.5	18.8	588	4	Q8WUX4	Q8wux4 homo sapien
23	348.5	18.8	613	4	Q96EY0	Q96ey0 homo sapien
24	348.5	18.8	613	4	Q8WUK1	Q8wuk1 homo sapien
25	348.5	18.8	614	4	Q96GA6	Q96ga6 homo sapien
26	348.5	18.8	618	4	Q96AA6	Q96aa6 homo sapien
27	347	18.7	613	11	Q8VCX7	Q8vcx7 mus musculus
28	329.5	17.8	227	6	Q28754	Q28754 ovis sp. lf
29	329.5	17.8	253	6	Q28753	Q28753 ovis sp. lf
30	319.5	17.2	159	6	Q28752	Q28752 ovis sp. lf
31	280.5	15.1	684	13	Q90544	Q90544 ginglymosto
32	272	14.7	384	4	Q9UP60	Q9up60 homo sapien
33	272	14.7	493	4	Q8NCL6	Q8ncl6 homo sapien
34	272	14.7	494	4	Q96K68	Q96k68 homo sapien
35	272	14.7	496	4	Q96KX8	Q96kx8 homo sapien
36	271.5	14.6	416	4	Q9NEP6	Q9nep6 homo sapien
37	269	14.5	496	4	Q96DK0	Q96dk0 homo sapien
38	269	14.5	499	4	Q8N5K4	Q8n5k4 homo sapien
39	267	14.4	497	4	Q8WY24	Q8wy24 homo sapien
40	267	14.4	500	4	Q9BRV0	Q9brv0 homo sapien
41	261	14.1	486	11	Q91Z07	Q91z07 mus musculus
42	261	14.1	487	11	Q99KA4	Q99ka4 mus musculus
43	260	14.0	426	11	Q9DCD9	Q9dcd9 mus musculus
44	253.5	13.7	481	11	Q91WT3	Q91wt3 mus musculus
45	253.5	13.7	481	11	Q91WT1	Q91wt1 mus musculus

ALIGNMENTS

RESULT 1

Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAh24289.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 388F7F4CF588660E CRC64;

Query Match 66.4%; Score 1233; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.7e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 121 DKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 180
Db 245 DKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 304
QY 181 GVEVHNKATPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240
Db 305 GVEVHNKATPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 364

241 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIATVWESNGOPENNYKTTTPPVLD 300
 365 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIATVWESNGOPENNYKTTTPPVLD 424

301 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 347
 425 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 471

RESULT 2

Q96PQ8 PRELIMINARY; PRT; 701 AA.
 Q96PQ8; 01-DEC-2001 (TrEMBLrel. 19, Created)
 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 Factor VII active site mutant immunoconjugate.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=21477448; PubMed=11593034;
 Hu Z., Garen A.;
 "Targeting tissue factor on tumor vascular endothelial cells and tumor
 cells for immunotherapy in mouse models of prostatic cancer.";
 Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
 -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 EMBL; AF272774; AAK58686.1; -.
 HSSP; P00761; IANI.
 InterPro; IPR000152; Asx_hydroxyl.
 InterPro; IPR001314; Chymotrypsin.
 InterPro; IPR000742; EGF_2.
 InterPro; IPR001681; EGF_CA.
 InterPro; IPR001438; EGF-II.
 InterPro; IPR006209; EGF-like.
 InterPro; IPR002383; GLA_blood.
 InterPro; IPR001110; Ig-like.
 InterPro; IPR003597; Ig-CL.
 InterPro; IPR003006; Ig-MHC.
 InterPro; IPR001254; Ser_protease_Try.
 InterPro; IPR000294; VitK_dep_GLA.
 Pfam; PF00008; EGF; 2.
 Pfam; PF00594; gla; 1.
 Pfam; PF00047; Ig; 2.
 Pfam; PF00089; trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 PRINTS; PR00010; EGFLOOD.
 PRINTS; PR00001; GLABLOOD.
 SMART; SM00179; EGF_CA; 1.
 SMART; SM00069; GLA; 1.
 SMART; SM00407; IGcl; 1.
 SMART; SM00020; Tryp_SPC; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 1.
 PROSITE; PS01187; EGF_CA; 1.
 PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 PROSITE; PS00835; IG-LIKE; 2.
 PROSITE; PS00290; IG-MHC; 1.
 PROSITE; PS02040; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 EGF-like domain; Hydrolase; Protease; Serine protease.
 SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 66.4%; Score 1233; DB 4; Length 701;
 Best Local Similarity 100.0%; Pred. No. 2.9e-100;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

121 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 180

Db 475 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 534
 QY 181 GVEVHNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 240
 Db 535 GVEVHNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 594
 QY 241 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIATVWESNGOPENNYKTTTPPVLD 300
 Db 595 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIATVWESNGOPENNYKTTTPPVLD 654
 QY 301 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 347
 Db 655 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 701

RESULT 3

Q8N4Y9 PRELIMINARY; PRT; 521 AA.
 ID Q8N4Y9
 AC Q8N4Y9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells from Tonsils;
 RA Strausberg R.;
 Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; BC033178; AAH33178.1;
 InterPro; IPR007110; Ig-like.
 InterPro; IPR003597; Ig-CL.
 InterPro; IPR003006; Ig-MHC.
 InterPro; IPR003596; Ig-V.
 Pfam; PF00047; Ig; 4.
 SMART; SM00407; IGcl; 3.
 SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG-LIKE; 4.
 DR PROSITE; PS00290; IG-MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 61.5%; Score 1142; DB 4; Length 521;
 Best Local Similarity 92.1%; Pred. No. 2.2e-92;
 Matches 209; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

121 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 180
 Db 295 DTTPPCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 354

QY 181 GVEVHNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 240
 Db 355 GVEVHNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 414

QY 241 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIATVWESNGOPENNYKTTTPPVLD 300
 Db 415 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIATVWESNGOPENNYKTTTPPVLD 474

QY 301 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 347
 Db 475 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 521

Query Match 66.4%; Score 1233; DB 4; Length 701;
 Best Local Similarity 100.0%; Pred. No. 2.9e-100;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

121 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 180

RESULT 4

Q8TC63 PRELIMINARY; PRT; 473 AA.
 ID Q8TC63
 AC Q8TC63;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 16:47:23 ; Search time 34.8701 Seconds
(without alignments)
421.045 Million cell updates/sec

Title: US-09-730-465-8

Perfect score: 1856

Sequence: 1 MVAGSDAGRALGVLSVVCLL.....MHEALHNHYTKSLSPGK 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgn2.6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2.6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2.6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2.6/ptodata/1/iaa/PCUS_COMB.pap.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1856	100.0	347	1	US-07-940-861-43
2	1856	100.0	347	1	US-08-459-512-43
3	1856	100.0	347	2	US-08-459-657-43
4	1856	100.0	347	2	US-08-460-132-43
5	1856	100.0	347	3	US-08-466-465-8
6	1856	100.0	347	5	PCT-US92-02050-43
7	1249	67.3	859	4	US-09-313-942-7
8	1249	67.3	1158	4	US-09-313-942-26
9	1249	67.3	1168	4	US-09-313-942-24
10	1247	67.2	446	4	US-09-157-452B-12
11	1242	66.9	388	3	US-09-131-247-16
12	1239.5	66.8	482	4	US-09-189-129-2
13	1239	66.8	442	5	PCT-US96-10043-9
14	1239	66.8	704	4	US-09-590-656-2
15	1239	66.8	704	4	US-09-733-764-2
16	1238.5	66.7	424	5	PCT-US95-03866-12
17	1238.5	66.7	424	5	PCT-US95-03866-14
18	1238.5	66.7	437	5	PCT-US96-10043-11
19	1238.5	66.7	691	4	US-09-313-942-20
20	1238.5	66.7	694	4	US-09-313-942-22
21	1238	66.7	680	3	US-08-227-496C-15
22	1237	66.6	229	4	US-09-122-144-2
23	1236	66.6	592	4	US-09-313-942-8
24	1235.5	66.6	488	3	US-08-776-511-2
25	1234	66.5	552	1	US-08-243-010-6
26	1233.5	66.5	694	4	US-09-313-942-18
27	1233.5	66.5	793	4	US-09-313-942-32

28	1233	66.4	232	2	US-08-595-043A-50
29	1233	66.4	235	3	US-09-131-247-6
30	1233	66.4	331	3	US-09-178-869-2
31	1233	66.4	331	4	US-09-761-413-2
32	1233	66.4	360	4	US-09-180-100-11
33	1233	66.4	371	1	US-08-236-311-7
34	1233	66.4	371	3	US-08-457-918-7
35	1233	66.4	376	4	US-09-180-100-22
36	1233	66.4	387	1	US-08-470-299-4
37	1233	66.4	389	3	US-09-131-247-14
38	1233	66.4	396	2	US-08-784-512-3
39	1233	66.4	396	3	US-09-176-228-3
40	1233	66.4	424	4	US-09-333-593A-8
41	1233	66.4	446	3	US-08-397-411-7
42	1233	66.4	449	1	US-08-458-516-13
43	1233	66.4	459	1	US-08-157-101A-7
44	1233	66.4	475	4	US-09-740-002-27
45	1233	66.4	476	2	US-08-378-939-10

ALIGNMENTS

RESULT 1

US-07-940-861-43
; Sequence 43, Application US/07940861
; Patent No. 5547853
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALINER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,861
; FILING DATE: 21-OCT-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151C1P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
JS-07-940-861-43

Query Match 100.0%; Score 1856; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 4.1e-163;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAGSDAGRALGVLSVVCLLHCFGFCFSCFQQIYGVVGNVTFHVPFVSNVPLKEVLKKQK 60
DB 1 MVAGSDAGRALGVLSVVCLLHCFGFCFSCFQQIYGVVGNVTFHVPFVSNVPLKEVLKKQK 60

QY 61 DKVAELENSEFRAPFSPKRVYLDVTSGSLTIYNLTSSDEDEYEMSPNITDTMKFFLYV 120
DB 61 DKVAELENSEFRAPFSPKRVYLDVTSGSLTIYNLTSSDEDEYEMSPNITDTMKFFLYV 120

QY 121 DKHTCPCPAPELLGGPSVFLPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVD 180
DB 121 DKHTCPCPAPELLGGPSVFLPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVD 180

QY 181 GVEVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240
DB 181 GVEVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240

QY 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGGOPENNYKTTTPVLD 300
DB 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGGOPENNYKTTTPVLD 300

QY 301 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 347
DB 301 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 347

RESULT 2

US-08-459-512-43
; Sequence 43, Application US/08459512
; Patent No. 5728677

GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,512
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-512-43

Query Match 100.0%; Score 1856; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 4.1e-163;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAGSDAGRALGVLSVVCLLHCFGFCFSCFQQIYGVVGNVTFHVPFVSNVPLKEVLKKQK 60
DB 1 MVAGSDAGRALGVLSVVCLLHCFGFCFSCFQQIYGVVGNVTFHVPFVSNVPLKEVLKKQK 60

QY 61 DKVAELENSEFRAPFSPKRVYLDVTSGSLTIYNLTSSDEDEYEMSPNITDTMKFFLYV 120
DB 61 DKVAELENSEFRAPFSPKRVYLDVTSGSLTIYNLTSSDEDEYEMSPNITDTMKFFLYV 120

QY 121 DKHTCPCPAPELLGGPSVFLPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVD 180
DB 121 DKHTCPCPAPELLGGPSVFLPPKPKDLMISRPEVTCVVVDVSHEDPEVKFNWYVD 180

QY 181 GVEVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240
DB 181 GVEVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 240

QY 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGGOPENNYKTTTPVLD 300
DB 241 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGGOPENNYKTTTPVLD 300

QY 301 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 347
DB 301 DGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 347

RESULT 3

US-08-459-512-43
; Sequence 43, Application US/08459657
; Patent No. 5914111

GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,657
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B151CIP2
; TELECOMMUNICATION INFORMATION: